

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: July 2, 2004, 10:27:16 ; Search time 3991 Seconds
(without alignments)
10871.054 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	997.8	99.7	9721	6	AX469435	AX469435 Sequence
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ALIGNMENTS

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LOCUS BD271230
DEFINITION Prediction of risk of interstitial lung disease.
ACCESSION BD271230
VERSION BD271230.1 GI:33080998
KEYWORDS JP 2002540801-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 9721)
AUTHORS Duff,G.W., Giovine,F.S.D. and Whyte,M.
TITLE Prediction of risk of interstitial lung disease
JOURNAL Patent: JP 2002540801-A 2 03-DEC-2002;

BD271230 9721 bp DNA linear PAT 17-JUL-2003
Prediction of risk of interstitial lung disease.

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VERSION	AX052806.1	GI:12226963		
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SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
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AUTHORS	Kornman, K.S., Duff, G.W., Crossman, D.C., Francis, S.E. and Stephenson, K.			
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JOURNAL	Patent: WO 0071753-A 16 30-NOV-2000; Interleukin Genetics, Inc. (US)			
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VERSION AX067266.1 GI:12544890
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Duff,G.W., Cox,A., Camp,N.J. and di Giovine,F.S.
JOURNAL Diagnostics and therapeutics for diseases associated with an il-1
PATENT: WO 0100880-A 2 04-JAN-2001;
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VERSION
AX469435.1 GI:21901721
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REFERENCE
1 Hill, J.A., Wang, Z.C., Anderson, D.J. and Yunis, E.J.
Variants of il-1 beta gene and cd46 gene for diagnosing unexplained
recurrent pregnancy loss
Patent: WO 0222877-A 1 21-MAR-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; DANA-FARBER CANCER
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DEFINITION
Methods of diagnosing and treating chronic obstructive airway
diseases.
ACCESSION
BD085856
VERSION
JP 2001522586-A
KEYWORDS
JP 2001522586-A/20.
SOURCE
unidentified
ORGANISM
unidentified
REFERENCE
1 (bases 1 to 9721)
Duff, G.W.; Giovain, M., Barnes, P.J. and Rim, S.
METHODS OF DIAGNOSING AND TREATING CHRONIC OBSTRUCTIVE AIRWAY
DISEASES.
PATENT: JP 2001522586-A 20-NOV-2001;
INTERLEUKIN GENETICS INC
OS Unidentified
PN JP 2001522586-A/20
PD 20-NOV-2001
PR 09-NOV-1998 JP 2000519607
PR 07-NOV-1997 GB 9723553.5, 12-JAN-1998 US 09/005923 PI
GORDON W DUFF, MARKO GIOVAIN, PETER J BARNES, SIMON RIM PC
C12N15/09, C12Q1/68, C12N15/00
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CC Topology: Linear;
CC Methods of diagnosing and treating chronic obstructive airway
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DEFINITION Human gene for prointerleukin 1 beta.
ACCESSION X04500
VERSION X04500.1 GI:33788
KEYWORDS interleukin 1 beta.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 9721)

Clark,B.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auron,P.E.

Genomic sequence for human prointerleukin 1 beta: possible

evolution from a reverse transcribed prointerleukin 1 alpha gene

Nucleic Acids Res. 14 (20), 7997-7914 (1986)

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3490654

Data kindly reviewed (13-MAY-1988) by Clark B.D.

Location/Qualifiers

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1809..1816

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1859..1866

TATA_signal

1903..1909

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1934..2005

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Best Local Similarity 99.8%; Pred. No. 2e-236;		
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
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DB	8405	AACAGAAGGTTTTGAGTAGCGGTATAGCTGGACTTCTGTTGTTCTACCAATGCC 8464
QY	121	CAACTGCTGCTTAGGTTAGGTTAGAGATCTCTGTTCCATCAGCCAGGACAGTCAG 180
DB	8465	CAACTGCTGCTTAGGTTAGGTTAGAGATCTCTGTTCCATCAGCCAGGACAGTCAG 8524
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DB	8525	CTCTCTCTTTTCAGGGCCAAATCCCGCCCTTTTGTGAGCCAGGCTCTCTCACCTTC 8584
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QY	901	CGCTATGCTAGGAGTGGGAGTACAGAGATGAGAAACAGTCAAGTCCCTCTCTCAGAT 960
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LOCUS Homo sapiens interleukin 1, beta (IL1B) gene, complete cds.		
DEFINITION AY137079		
ACCESSION AY137079		
VERSION AY137079.1 GI:22122009		
KEYWORDS Homo sapiens (human)		
SOURCE Homo sapiens		
ORGANISM Homo sapiens		
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS Rieder M.J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldane, S.A.,		
Rajkumar, N.R., Toth, E.J., Yi, Q. and Nickerson, D.A.		
TITLE Direct Submission		
JOURNAL Submitted (29-JUN-2002) Genome Sciences, University of Washington,		
1705 NE Pacific, Seattle, WA 98195, USA		
COMMENT To cite this work please use: SeattleSNPs. NHLBI HL66682 Program		
for Genomic Applications, UW-PHCRC, Seattle, WA (URL:		
http://pga.gs.washington.edu).		
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QY 891 GTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCACAAGTCC 950
DB 8634 GTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCACAAGTCC 8693

QY 951 CTCCTCAGATAGGAGAGCGAGCTAGTTATATAGCAG-AACAAGGTAACATGAC 1001
DB 8694 CTCCTCAGATAGGAGAGCGAGCTAGTTATATAGCAGAAACAGGTAACATGAC 8745
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RESULT 8
AC079753/c
LOCUS      154214 bp      DNA      linear      PRI 01-MAR-2002
DEFINITION Homo sapiens BAC clone RP11-67L14 from 2, complete sequence.
ACCESSION  AC079753
VERSION    AC079753.7 GI:14318395
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 154214)
AUTHORS   Sulston, J.E. and Waterston, R.
TITLE     Toward a complete human genome sequence
JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE   99063792
PUBMED    9847074
REFERENCE  2 (bases 1 to 154214)
AUTHORS   Andrews, S., Cotton, M., Doebber, A. and Rose, C.
TITLE     The sequence of Homo sapiens BAC clone RP11-67L14
JOURNAL   Unpublished (2001)
REFERENCE  3 (bases 1 to 154214)
AUTHORS   Waterston, R.H.
TITLE     Direct Submission
JOURNAL   Submitted (10-SEP-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE  4 (bases 1 to 154214)
AUTHORS   Waterston, R.H.
TITLE     Direct Submission
JOURNAL   Submitted (06-JUN-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE  5 (bases 1 to 154214)
AUTHORS   Waterston, R.H.
TITLE     Direct Submission
JOURNAL   Submitted (03-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE  6 (bases 1 to 154214)
AUTHORS   Waterston, R.
TITLE     Direct Submission
JOURNAL   Submitted (09-JAN-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE  7 (bases 1 to 154214)
AUTHORS   Waterston, R.
TITLE     Direct Submission
JOURNAL   Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On Jun 6, 2001 this sequence version replaced gi:14029079.
            ----- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: sapiens@watson.wustl.edu
            ----- Summary Statistics
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            Center project name: H_NH0067L14
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Matches 962; Conservative 0; Mismatches 38; Indels 12; Gaps 7;

QY 1 GCTGTACCCAGAGAGTCTGCTGTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 60
Db |||||
45765 GCTGTACCCAGAGAGTCTGCTGTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 45706
QY 61 AACAGAAAGGTTTTGAGTAGTACGGCTATAGCTGTGAGCTTTCTCTGTTGTCTACCAATGCC 120
Db |||||
45705 AACAGAAAGGTTTTGAGTAGTACGGCTATAGCTGTGAGCTTTCTCTGTTGTCTACCAATGCC 45646
QY 121 CAATCTGCTGCTTAGGCTAGTGTAGAGAGTCTCTGTCCATCAGCAGGACAGTCAG 180
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QY 181 CTCTCTCTCTTTAGGGGCAATCCCGAGCCCTTTTGTAGCCAGGCTCTCTCACTCTC 240
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QY 241 CTACTCACTTAAGCCGCTGACAGAAACCGGCCACATTTGGTCTTAAGAAACCCCTC 300
Db |||||
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45465 TGTCAATTCGCTCCACATCTCTGATGAGCAACCGCTTCCCTCTATTTATTTATTTGTTT 45406
QY 361 GTTTGTTTTGATTCATTTGATTAATTTATTAAGAGGAGGAGAGTAGAGTGTCTGTA 420
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45405 GTTTGTTTTT-ATTCATTTGTTT-ATTCATTTGTTT-ATTCATTTGTTT-ATTCATTTGTTT 45347
QY 421 AAGAGGCTAGTTTTTAATAGCTATGAATCAATTTCAATTTGAGCTGGTGTCTCTTT 480
Db |||||
45346 AAGAGGCTAGTTTTTAATAGCTATGAATCAATTTGAGCTGGTGTCTCTTT 45287
QY 481 AAATCAAGTCTCTTTAAATTAACACTGAAATATATATAAGCTCAGATTTATTAATGGGAATA 540
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Db |||||
45226 TTTTAAATAGCAAAATATGATCTGTTCAATGTTCTGAATTAATTAATTAATTAATTAATTAAT 45167
QY 601 AAAAAAAGGGTCTCTCTGATCAATGACTGTCTGATTTGACACTGA- - -CAGTAAGC 656
Db |||||
45166 AAAAAAGGGTCTCTCTGATCAATGACTGTCTGATTTGACACTGAACAGTAAGACA 45107
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Db |||||
45106 AAACAGGCTGTGAGAGTTCTTTGGGGGACTAAAGGCCACTCTCAATGCTGAGTCTGC-A 45047
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Db |||||
45046 AGTACCTAGAAATATCTTTGGCCACCGAAGACTATCTCTCTCAACCATCCCTTTATTTTC 44987
QY 773 -GTTGTTCAACAGAAAGGATATCTAGTGCACATCTGGAACAGGATCAGCTGAAGCAGTGA 831
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44986 TGTGTTTCAACAGAAAGGATATCTAGTGCACATCTGGAACAGGATCAGCTGAAGCAGTGA 44927
QY 832 GGGAGTCAGGACTGGTAGTACAGCTACCA-TGATTTTATCTATCAATGACACCAACATCT 890
Db |||||
44926 GGGAGTCAGGACTGGTAGTACAGCTACCA-TGATTTTATCTATCAATGACACCAACATCT 44867
QY 891 GTTGAAGCAAGCCCTATGATCTAGGAGTGGAGTACAGAGATGAGACAGTCAAGTCC 950
Db |||||
44866 GTTGAAGCAAGCCCTATGATCTAGGAGTGGAGTACAGAGATGAGACAGTCAAGTCC 44807
QY 951 CTCCTCAGATAGGAGGAGCCCTAGTTATAGCAG-AACAGGTAACATGAC 1001
Db |||||
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LOCUS BD080414 176373 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel molecules of the Tango-77 related protein family and uses thereof.
ACCESSION BD080414
VERSION BD080414.1 GI:22626017
KEYWORDS JP 2001512002-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Pan, Y.
REFERENCE 1 (bases 1 to 176373)
AUTHORS Novel molecules of the Tango-77 related protein family and uses
TITLE Patent: JP 2001512002-A 6 21-AUG-2001;
JOURNAL MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2001512002-A/6
PD 21-AUG-2001
PF 03-AUG-1998 JP 2000505182
PR 04-AUG-1997 US 60/054646, 02-JUL-1998 US 60/091650 PI
YANG PAN
PC C12Q1/68, C07K14/52, C07K16/24, C12N5/10, C12N15/09, C12P21/02, PC
C12Q1/02,
PC G01N33/15, G01N33/50, G01N33/53, G01N33/53, G01N33/566//A61K31/ PC
708B, A61K38/00,
PC A61P3/10, A61P11/06, A61P19/02, A61P29/00, A61P37/02, C12N5/00, PC
C12N15/00,
PC A61K37/02
CC n = A,T,C or G Location/Qualifiers
FH misc Location/Qualifiers
FT misc Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 95.8%; Pred. No. 1.7e-199;
Matches 972; Conservative 0; Mismatches 24; Indels 19; Gaps 9;
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Db 136209 GCTGTACCCAGAGAGTCTCTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 136150
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QY 241 CTACTCACTTAAAGCCGCTGACAGAAACCGGCCACATTTGGTCTTAAGAAACCCCTC 300
Db 135969 CTACTCACTTAAAGCCGCTGACAGAAACCGGCCACATTTGGTCTTAAGAAACCCCTC 135910
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Db 135909 TGTCAATTCGCTCCACATCTCTGATGAGCAACCGCTTCCCTCTATTTATTTATTTGTTT 135850
QY 361 GTTTGTTTTGATTTCAATTTGTTTCTAATTTATTTCAAAGGGGCAAGAGTAGTGTCTGTA 420
Db 135849 GTTTGTTTT-ATTCATTTGTTT-ATTCATTTGTTT-ATTCATTTGTTT-ATTCATTTGTTT 135791
QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGAGTGTGTCTCTTT 480
Db 135790 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGAGTGTGTCTCTTT 135731

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QY 481 AATCAAGTCCCTTTAAATTAACACCTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
Db 135730 AATCAAGTCCCTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 135671
QY 541 TTTTAAATGAGCAAAATATGATATCTGTTCAATGTTCTGAAATAAATTTCACTGAAAGAA 600
Db 135670 TTTTAAATGAGCAAAATATATCATCTGTTCAATGTTCTGAAATAAATTTCACTGAAAGAA 135611
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Db 135610 AAAAAA---GGTCTTTCCCTGATCATTTGACCTGTTGGAATTTGACACTGAACAGTAAAG 135555
QY 654 AGCAAAAGGCTGTGAGAGTCTTTGGG---ACTAAGCCCACTCTCTCAATGCTGAGTCTG 710
Db 135554 ACAAAACAGGGCTGTGAGAGTCTTTGGGGAGCTAAAGCCCACTCTCTCAATGCTGAGTCTG 135495
QY 711 C-AAGTACCTAGAAATATCTTTGGCCACCGAAGACTATCTCTCACCCTCCCTTTAT 769
Db 135494 CAAGTACCTAGAAATATCTTTGGCCACCGAAGACTATCTCTCACCCTCCCTTTAT 135435
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RESULT 10
AX774856
LOCUS AX774856 7824 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 172 from Patent WO03038129.
ACCESSION AX774856
VERSION AX774856.1 GI:32486372
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
1.
AUTHORS Raponi, M.
TITLE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 172 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
FEATURES
Location/Qualifiers
1..7824
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ORIGIN

Query Match 83.4%; Score 834.6; DB 6; Length 7824;
Best Local Similarity 94.2%; Pred. No. 5.5e-196;
Matches 956; Conservative 0; Mismatches 44; Indels 15; Gaps 8;
QY 1 GCTGTACCCAGAGAGTCCCTGCTGATGTGGACTCAATCCCTAGGCTGGCGAAGAGG 60
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QY 61 AACAGAAAGGTTTTTTCAGTACGCGCTATAGCCTGGACTTTTCTGTTGTCTACACCAATGCC 120
Db 6848 AACAGAAAGGTTTTTTCAGTACGCGCTATAGCCTGGACTTTTCTGTTGTCTACACCAATGCC 6907
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QY 121 CAACTGCCTGCCCTTAGGGTAGTCTAAGAGGATCTCCTGTCATCAGCCAGGACAGTCAG 180
Db 6908 CAACTGCCTGCCCTTAGGGTAGTCTAAGAGGATCTCCTGTCATCAGCCAGGACAGTCAG 6967
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Db 7627 GCAGGAGTCAAGGCTGTGATTAACAGCTACCA-TGATTTATCTATCAATGACCAACA 7686
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RESULT 11

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LOCUS HUMILIB 7824 bp DNA linear PRI 09-AUG-1995
DEFINITION Human interleukin 1-beta (IL1B) gene, complete cds.
ACCESSION M15840
VERSION M15840.1 GI:186281
KEYWORDS Alu repeat; interleukin 1-beta.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 7824)
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Qy	829	GCAGGAGTCAGCACTGGTAGTAAACAGTACCA-TGATTTATCTATCAATGCACCAACA	887					
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Qy	888	TCGTGTTGACCAACGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGACAGTCAAG	947					
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Qy	948	TCCTCTCCTCAGATAGGAGGAGCTAGTTATAAGCAG-AACAAGGTAAACATGAC	1001					
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RESULT 12								
LOCUS	BD080413/c	152331 bp	DNA linear PAT 27-AUG-2002					
DEFINITION	Novel molecules of the Tango-77 related protein family and uses thereof.							
ACCESSION	BD080413							
VERSION	BD080413.1	GI:22626016						
KEYWORDS	JP 2001512002-A/5.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	Pan,Y.							
TITLE	Novel molecules of the Tango-77 related protein family and uses							
JOURNAL	Patent: JP 2001512002-A 5 21-AUG-2001;							
COMMENT	MILLENNIUM PHARMACEUTICALS INC OS Homo sapiens (human) PN JP 2001512002-A/5 PD 21-AUG-2001 PF 03-AUG-1998 JP 2000505182 PR 04-AUG-1997 US 60/054646,02-JUL-1998 US 60/091650 PI YANG PAN PC C12Q1/68,C07K14/52,C07K16/24,C12N5/10,C12N15/09,C12P21/02, PC C12Q1/02, PC GOIN33/15,GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566//A61K31/ PC 7088,A61K38/00, PC A61P3/10,A61P11/06,A61P19/02,A61P29/00,A61P37/02,C12N5/00, PC C12N15/00, PC A61K37/02 CC n = A,T,C or G FH Key Location/Qualifiers FT misc feature (1)..(152331).							
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Best Local Similarity 90.9%; Pred. No. 7.2e-140;								
Matches 769; Conservative 0; Mismatches 62; Indels 15; Gaps 11;								
Qy	170	AGGACAGTCAGCTCTCTCTCTTTGAGGCAATCCCGAGCCCTTTTGTGTGACGAGCCCTC	229					
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Qy	230	TCTCAGCTCTCTTACTCTACTTAAAGCCGCGCTGACAGAAACACGAGCCCACTTTGGTTCT	289					
Db	120873	TCTCAGCTCTCTTACTCTACTTAAAGCAACGCGCTTTCAGGACATCCCGAGCCCTTT	120814					
Qy	290	AAGAAACCCCTCTGTCTATTCGCTCCCACTCTGTATGAGCAACCGCTTCCCTATTATTATTA	349					
Db	120813	AGAARACCCCTCTGTCTATTCGCTCCCACTCTGTATGAGCAACCGCTTCCCTATTATTATTA	120754					
Qy	350	TTTATTTGTTGTTGTTGTTTGAATCAATGGTCTTAATTTATTCAAAGGGGCAAGATGAG	409					
Db	120753	TTTATTTGTTGTTGTTGTTT-ATTCAATGGTCTTAATTTATTCAAAGGGGCAAAAGTAT	120695					

Qy	410	CAGTGTCTGTAAGAACCTAG-TTTTAAATAGCTATGGAATCAATCAATTTGGACTGG	468
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Qy	469	TGTGCTCTCTTTAAATCAAGTCCTTTAAATTAACACTGGAATATATAGCTCAGATTAT-T	527
Db	120634	TGTGCTCTCTTTAAATCATGTCCTTTTAAATACGACTGAAATATATCTGCTCCGATCATTT	120575
Qy	528	TTAAATGGGAATATTTAT-AAATCAGCAAAATATGATACTGTTTCAATGCTTCTGAAATATA	586
Db	120574	TTAAGTGGGAATATTTATGAAATTTACCAATATCATACTGTTTCAATGATTTCTGAAATATA	120515
Qy	587	CTTCACCTGAAGAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACT	646
Db	120514	CTTCACCTGAAGAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACT	120455
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Qy	700	GCTGAGTGTGTC-AAGTACCTAGAAAAATTCCTTGGCCACCGAAGACTATCTCTCTCACCC	758
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Db	120334	ATCCCCCTTTATTCCTTGTTCACAGAGGATATTCAGTGCAATCTGGAAACAGATCA	120275
Qy	818	GCTGAAGCACTGCAGGAGTCAGACTGGTAGTAACAGCTACCA-TGATTTATCTATCAA	876
Db	120274	GCTGAAGCACTGCAGGAGTCAGACTGGTAGTAACAGCTACCAAGTATTTATCTATCAA	120215
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Db	120154	ACAGTCACAAGTCCTCTCTCAGATAGGAGGCGAGCTAGTTTATAGCAGAAACAAGGTAA	120095
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Db	120094	CATGAC 120089	
RESULT	13		
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LOCUS		614 bp DNA linear STS 15-AUG-1995	
DEFINITION		human STS CHLC.UTR_00699_X04500.P37183 clone UTR_00699_X04500,	
		sequence tagged site.	
ACCESSION		G10509	
VERSION		G10509.1 GI:942358	
KEYWORDS		STS; STS sequence; primer; sequence tagged site.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 614)	
JOURNAL		Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.	
COMMENT		Cooperative Human Linkage Center	
		Unpublished (1995)	
		Synonyms: UTR_00699_X04500, CHLC.UTR_00699_X04500.T35097	
		Contact: Dr. Jeffrey C. Murray	
		UoI	
		The University of Iowa	
		Department of Pediatrics, Iowa City, IA 52242, USA	
		Tel: (319) 356-3508	
		Fax: (319) 356-3347	
		Email: jeff-murray@uiowa.edu	
		Primer A: AGTCAGCTCTCTCTTTTCAGG	
		Primer B: CTTGCCCTTTTGAATTAAT	
		STS size: 229	

Primer A: AGTCAGCTCTCTCCTTCAGG
Primer B: CTGCCCCCTTGAATAAT
STS size: 229

PCR Profile:

denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C

Protocol:

Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 ul

Buffer:

MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3

Prepared with primer pairs derived from X04500.

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
180..408
180..200
complement(389..408)

FEATURES

source
STS
primer_bind
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ORIGIN

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Best Local Similarity 99.7%; Pred. No. 2.9e-139;
Matches 607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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181 CTCTCTCTTTTACGGCCCAATCCCGACCCCTTTTGTGAGCCAGGCTCTCTACCTCTC 240
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241 CTACTCACTTAAAGCCGCCCTGACAGAAACCCAGGCCACATTTGGTCTTAAGAAACCCCTC 300
246 CTACTCACTTAAAGCCGCCCTGACAGAAACCCAGGCCACATTTGGTCTTAAGAAACCCCTC 305
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306 TGTCATTCGCTCCACATCTGTATGAGCAACCGCTTCCTCTATTATTATTATTATTGTTT 365
361 GTTTGTTTTGATTCATTCGCTCTAATTTATTTCAAGGGGGGCAAGTAGCAGTCTGTGA 420
366 GTTTGTTTTGATTCATTCGCTCTAATTTATTCAGAGGGGGCAAGTAGCAGTCTGTGA 425
421 AAAGAGCCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTT 480
426 AAAGAGCCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTT 485
481 AAATCAAGTCTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 540
486 AAATCAAGTCTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 545
541 TTTTAAATGAGCAATATGATCTGTTTCAATGGTCTGAAATAACTTCACTGAAGAAA 600
546 TTTTAAATGAGCAATATGATCTGTTTCAATGGTCTGAAATAACTTCACTGAAGAAA 605

QY

601 AAAAAAAAAA 609
|||||
606 AAAAAAAAAA 614

Db

RESULT 14

BC008678

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1522 bp mRNA linear PRI 04-OCT-2003
Homo sapiens interleukin 1, beta, mRNA (cdna clone MGC:9216
IMAGE:3875593), complete cds.

BC008678
BC008678.1 GI:14250476
MGC.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1522)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Shat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaeetz, T.E., Brownstein, M.J., Udwin, T.B., Toshivuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 1522)
Strausberg, R.
Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Speed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 13 Row: 6 Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 27894305.

FEATURES

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QY 481 AAATCAAGTCTTTAAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
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Db 1502 AAAAAAAAA 1510

RESULT 15
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LOCUS
DEFINITION Human mRNA for prointerleukin 1 beta.
ACCESSION X56087
VERSION X56087.1 GI:35662
KEYWORDS prointerleukin 1; prointerleukin 1 beta.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1473)
Kotenko,S.V., Bulenkov,M.T., Veiko,V.P., Epishin,S.M.,
Lomakin,I.B., Emel'yanov,A.V., Kozlov,A.P., Konusova,V.G.,
Kotov,A.Y., Kurbatova,T.V., Reshetnikov,V.L., Simbirtsev,A.S.,
Ketlinkii,S.A. and Vinetskii,Y.P.
Cloning of the cDNA coding for human prointerleukin-1 alpha and
prointerleukin-1 beta
Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989)
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PUBMED
2635664
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Best Local Similarity 98.8%; Pred. No. 5.6e-133;
Matches 595; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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DB 873 GCTGTACCCAGAGTCTGTGCTGATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 932
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DB 933 AACAGAAAGTGTGTGAGTACGGCTATAGCTGACTTTCCTGTGTGTCTACACCAATGCC 992
QY 121 CAATGCTGCTTAGGGTAGTGTAAAGAGATCTCTGTCCATCAGCCAGGACAGTCAG 180
DB 993 CAATGCTGCTTAGGGTAGTGTAAAGAGATCTCTGTCCATCAGCCAGGACAGTCAG 1052
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DB 1053 CTCTCTCTTTTACGGGCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 1112
QY 241 CTACTCACTTAAGCCCGCTGACAGAAACAGCGGCCACATTTGGTGTCTAAGAAACCCCTC 300
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1113	Db	CTACTCACTTAAGCCGCGCTGACAGAAACCGGCCACATTTGGTCTTAAGAAACCCCTC	1172
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421	Qy	AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTCAAATTTGGACGTGGTGTCTCTCTTT	480
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601	Qy	AA 602	
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Search completed: July 2, 2004, 12:34:03
Job time : 3999 secs

2
4
6

7 XX
8 XX

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Claim 34; Fig 2; 74pp; English.

The present sequence is that of human interleukin-1 beta (IL-1B) allele 2 (+6912), which is a form of the IL-1B gene that contains guanine at position +6912; IL-1B allele 1 (+6912) has cytosine at this position (see ARA50174). The invention is based on the identification of this novel allele at marker +6912 of the IL-1B gene. The C to G transition occurs within the 3' untranslated region of the IL-1B gene and results in an increased level of IL-1B protein. Individuals homozygous for the IL-1B allele 2 (+6912) accumulate approximately 4 times more immunoreactive IL-1B protein than homozygotes for IL-1B allele 1 (+6912). Methods and kits are provided for detecting IL-1B allele 2 (+6912), or an allele in linkage disequilibrium with an IL-1B allele 2 (+6912), and thereby determining a patient's susceptibility to developing inflammatory disorders, especially coronary artery disease, osteoporosis, nephropathy in diabetes mellitus, alopecia areata, graves disease, systemic lupus erythematosus, lichen sclerosis, ulcerative colitis, diabetic retinopathy, periodontal disease, juvenile chronic arthritis, psoriasis, insulin dependent diabetes, asthma, chronic inflammatory liver disease, chronic inflammatory lung disease, lung fibrosis, and rheumatoid arthritis (claimed). Identification of the IL-1B allele 2 (+6912) and its involvement in IL-1B overproduction also enables screening assays for identifying IL-1B antagonists that can be used to treat conditions associated with IL-1B allele 2 (+6912). Transgenic animals are also claimed, and can be used to identify IL-1B agonists and antagonists, or to confirm the safety and efficacy of candidate therapeutics.

Sequence 9721 BP: 2661 A: 2327 C: 2123 G: 2608 T: 0 U; 2 Other;

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1	GCTGTACCCAGAGAGTCTGTGCTCAATGTGGACTCAATCCCTAGGCTGCAGAAAGG	60				
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121	CAACTGCCTGCCTTAGGTTAGTGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG	180				
8465	CAACTGCCTGCCTTAGGTTAGTGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG	8524				
191	CTCTCTCCTTTTCAGGGCAATCCCGCGCCTTTTGTGAGCCAGGCTCTCTCACCTCTC	240				
8525	CTCTCTCCTTTTCAGGGCAATCCCGCGCCTTTTGTGAGCCAGGCTCTCTCACCTCTC	8584				
241	CTACTCACTTAAAGCCGCCCTGACAGAAACACCGGCCACATTTGGTTCTTAAGAAACCTC	300				
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8705	GTTTGTGTTTGATTCATTGGTCTAATTTATTTCAAAGGGGGGCAAGAGTAGCAGTGTCTGTA	8764				
421	AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTTGGACTGGTGTGCTCTCTTT	480				
8765	AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTTGGACTGGTGTGCTCTCTTT	8824				
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8825	AAATCAAGTCCTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGATA	8884				
541	TTTTAAATGAGCAATATGATCTGTTCAAATGGTTCGAAATAAACTTCACTGAAGAAA	600				
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Qy	841	GACTGTGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAAACATCTGTTTGACCAAG	900
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RESULT 2
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DT 29-JUL-1999 (first entry)

Human interleukin 18 gene.

Human; interleukin 1; IL-1B; IL-1A; IL-1PN; diagnosis; detection;
KW
chronic obstructive airway disease; chronic bronchitis; emphysema;
KW
asthma; chronic bronchiolitis; proinflammatory haplotypes; ss.
KW

XX Homo sapiens

XX PN WQ9924615-A2.

20-MAV-1999

09-NOV-1998: 98W0-IIS023721.

XX
PR 07-NOV-1997: 97GB-00023553.

PK XX
12-JAN-1998; 2005-00003323.

FA (MEDI- / MEDICAL SCI SYSTEMS INC.
XX

[illegible]

XX
XX
DK
WFI; 1999-321420/21.

PT genotyping nucleic acid samples by microarray technology for predicting susceptibility to developing chronic obstructive airway disease.

Example 1: Fig 2: 37pp: English.

xx The present invention describes genotyping a nucleic acid sample from a
cc subject to determine at least one allele of an interleukin-1 (IL-1)
cc proinflammatory haplotype. A method has also been described for
cc determining a subject's susceptibility to developing chronic obstructive
cc airway disease (COAD) or for predicting the rapidity or ultimate
cc progression of a COAD in the subject by: (a) obtaining a nucleic acid
cc sample from the subject; and (b) detecting at least one allele of an IL-

CC proinflammatory haplotype in the sample, where detection of at least one
CC of these alleles indicates that the patient has an increased
CC susceptibility to developing COPD. The method is useful for determining
CC the susceptibility of subjects to developing chronic obstructive airway
CC disease or for predicting the rapidity or ultimate progression of chronic
CC obstructive airway disease (COPD). COPD can be asthma, emphysema, chronic
CC bronchitis or chronic bronchiolitis. The method provides for early
CC identification of chronic obstructive airway disease (COPD), facilitating
CC administration of appropriate treatment at the earliest stage, thereby
CC increasing the probability of a positive outcome. The present sequence
CC represents the human IL-1B gene
XX

SQ Sequence 9721 BP; 2662 A; 2328 C; 2121 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 2; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGTACCCAGAGTCTCTGCTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
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QY 601 AAAAAAAGAGGTCTCTCTGATCATTTGACTGTCTGGAATGACACTGACAGTAAGCAAAAC 660
DB 8945 AAAAAAAGAGGTCTCTCTGATCATTTGACTGTCTGGAATGACACTGACAGTAAGCAAAAC 9004

QY 661 AGGCTGTAGAGTTCTTTGGGACTAAGCCCACTCTCTATTCCTGAGTGTCTCAAGTACCTA 720
DB 9005 AGGCTGTAGAGTTCTTTGGGACTAAGCCCACTCTCTATTCCTGAGTGTCTCAAGTACCTA 9064

QY 721 GAAATATCTTGGCCACCGAGACTATCTCTCTCACCCTATCCCTTTATTTGTTGTTCA 780
DB 9065 GAAATATCTTGGCCACCGAGACTATCTCTCTCACCCTATCCCTTTATTTGTTGTTCA 9124

QY 781 ACAGAGGATATTCAGTGCATCTGGAACAGGATAGCTGGAACACTGACGGAGTCTAG 840
DB 9125 ACAGAGGATATTCAGTGCATCTGGAACAGGATAGCTGGAACACTGACGGAGTCTAG 9184

QY 841 GACTGTGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAAACATCTGTTGAGCAAG 900
DB 9185 GACTGTGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAAACATCTGTTGAGCAAG 9244

QY 901 CGCTATGTACTAGAGCTGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCTCAGAT 960
DB 9245 CGCTATGTACTAGAGCTGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCTCAGAT 9304

QY 961 AGGAGAGGAGCTAGTATTATAAGCAGAACAGGTAACATGAC 1001
DB 9305 AGGAGAGGAGCTAGTATTATAAGCAGAACAGGTAACATGAC 9345

RESULT 3

ABX15529

ID ABX15529 standard; DNA; 9721 BP.

XX ABX15529;

XX 11-APR-2003 (first entry)

XX Human interleukin-1B, IL-1B, gene.

XX Human; ds: gene; interleukin-1B; IL-1B; chromosome 2q13; nephropathy;
XX inflammatory disease; Systemic Inflammatory Response; SIRS;
XX Alzheimer's disease; arthritis; acute joint inflammation; ophthalmopathy;
XX juvenile chronic arthritis; asthma; bronchial asthma; pulmonary disease;
XX chronic obstructive airways disease; cardiovascular disease; thyroiditis;
XX atherosclerosis; autoimmune carditis; cardiomyopathy; ulcerative colitis;
XX cardiac cell dysfunction; aortic smooth muscle cell activation; trauma;
XX inflammatory bowel disease; gastrointestinal inflammation; cerebral trauma;
XX Kawasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy;
XX glomerulonephritis; diabetic retinopathy; Grave's ophthalmopathy;
XX osteoporosis; bone loss; otitis media; pancreatitis; periodontal disease;
XX chronic lung disease; chronic sinusitis; chronic lymphocytic thyroiditis;
XX urinary tract infection; chronic prostatitis; immunological disorder;
XX chronic pelvic pain syndrome; alopecia areata; Grave's disease;
XX thyroid disease; goiter; struma lymphomatosa; sleep disorder; neoplasia;
XX chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis;
XX Leprosy; myocardial dysfunction; breast cancer; organ transplant;
XX Hodgkin's disease; hormonal regulation; fertility; septicaemia.

XX Homo sapiens.

XX US2002146700-A1.

XX 10-OCT-2002.

XX 27-APR-2001; 2001US-00845129.

XX 29-MAY-1997; 97GB-00011040.

XX 30-JUN-1999; 99US-00345217.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Duff GW, Cox A, Camp NJ, Di Giovine PS;

XX WPI; 1999-080814/07.

XX New method of determining a patient's susceptibility to inflammatory
XX disorders - by detecting the presence of an IL-1 (4412332) haplotype,
XX useful in designing treatment strategies that modulate the activity of
XX proteins produced by the IL-1 gene cluster.

XX Disclosure; Fig 4; 42pp; English.

XX The invention relates to a method for determining whether a subject has
XX or is predisposed to developing a disease or condition that is associated
XX with an IL-1 inflammatory haplotype. The method involves detecting at
XX least one allele of the haplotype, where the presence of the allele
XX indicates that the subject is predisposed to the development or has the

disease or condition. The invention allows the determination of an individual's likelihood for developing a particular disease or condition associated with interleukin 1 (IL-1) polymorphisms without necessarily determining or characterising the causative genetic variation. Diseases such as inflammatory disease e.g. Systemic Inflammatory Response (SIRS), Alzheimer's disease, arthritis e.g. acute joint inflammation, juvenile chronic arthritis, asthma e.g. bronchial asthma, chronic obstructive airways disease, cardiovascular diseases e.g. atherosclerosis, autoimmune carditis, cardiomyopathy and cardiac cell dysfunction e.g. aortic smooth muscle cell activation, cardiac cell apoptosis, gastrointestinal inflammation e.g. inflammatory bowel disease, ulcerative colitis, HIV infections, Kawasaki's syndrome e.g. cervical lymphadenopathy, coronary artery lesions, nephropathies e.g. diabetic retinopathy, Grave's disease, glomerulonephritis, ophthalmopathies e.g. diabetic media; pancreatitis; ophthalmopathy; osteoporosis e.g. bone loss, ocular media; pancreatitis; periodontal disease; pulmonary diseases e.g. chronic lung disease, chronic sinusitis; thyroiditis e.g. chronic lymphocytic thyroiditis; urinary tract infections e.g. chronic prostatitis, chronic pelvic pain syndrome; immunological disorders e.g. alopecia areata, Graves disease; thyroid diseases e.g. goiter, struma lymphomatosa; sleep disorders; chronic fatigue syndrome; obesity; infectious diseases e.g. Leprosy, Leishmaniasis; trauma e.g. cerebral trauma, myocardial dysfunction; neoplasias e.g. breast cancer, Hodgkin's disease; hormonal regulation e.g. fertility, septicemia; organ transplants. This allows for a more customised approach to preventing the onset or progression of the disease or condition, e.g. a clinician can more effectively prescribe a therapy that will address the molecular basis of the disease or condition. The present sequence represents the sequence of the human interleukin-1B gene located on chromosome 2q13

Sequence 9721 BP; 2651 A; 2329 C; 2121 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 2; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGTACCCAGAGCTCTGTGCTGAATGTGACATCAATCCCTAGGGCTGCAGAAAGGG 60
DB 8345 GCTGTACCCAGAGCTCTGTGCTGAATGTGACATCAATCCCTAGGGCTGCAGAAAGGG 8404

QY 61 AACAGAAAGTTTTTGAGTACGGCTATAGCCCTGGACTTTCTGTGTGTACACCAATGCC 120
DB 8405 AACAGAAAGTTTTTGAGTACGGCTATAGCCCTGGACTTTCTGTGTGTACACCAATGCC 8454

QY 121 CAATGCTGCTTCTAGGTAGTCTTAAGAGATCTCTGTCCATCAGCAGCAGAGTCAG 180
DB 8465 CAATGCTGCTTCTAGGTAGTCTTAAGAGATCTCTGTCCATCAGCAGCAGAGTCAG 8524

QY 181 CTCTCTCTCTTCAGGGCCCAATCCCGAGCCCTTTCTGTGAGCCAGCCCTCTCTACCTCTC 240
DB 8525 CTCTCTCTCTTCAGGGCCCAATCCCGAGCCCTTTCTGTGAGCCAGCCCTCTCTACCTCTC 8594

QY 241 CTACTCACTTAAGCCCGCTGACGAAACACAGCCCAATTTGGTCTTACGAACCTCT 300
DB 8585 CTACTCACTTAAGCCCGCTGACGAAACACAGCCCAATTTGGTCTTACGAACCTCT 8644

QY 301 TGTCTATCCCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
DB 8645 TGTCTATCCCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704

QY 361 GTTTGTTTTGATTCATTTGTTCTTAATTTATTAAGGGGGCAAGAGTAGCGTGTCTGTA 420
DB 8705 GTTTGTTTTGATTCATTTGTTCTTAATTTATTAAGGGGGCAAGAGTAGCGTGTCTGTA 8764

QY 421 RAAGAGCCCTAGTTTTTAATAGTATGGATCAATTTCAATTTGGTGTGTCTCTCTTT 480
DB 8765 RAAGAGCCCTAGTTTTTAATAGTATGGATCAATTTGGTGTGTCTCTCTTT 8824

QY 481 AAATCAAGTCCTTTTAATTAACACTGAAATATATATAGCTCAGATTATTAAATGGGAATA 540
DB 8825 AAATCAAGTCCTTTTAATTAACACTGAAATATATATAGCTCAGATTATTAAATGGGAATA 8884

QY 541 TTTATAATGACCAATATGACTGTTTCAATGGTTCTGAAATAACTTCACCTGAAGAA 600

8885 TTTATAATGACCAATATGACTGTTTCAATGGTTCTGAAATAACTTCACCTGAAGAA 8944
601 AAAAAAAGGGTCTCTCTGATCATTTGATCTGTCTGGATTGACATGACATGAAGCAAC 660
8945 AAAAAAAGGGTCTCTCTGATCATTTGATCTGTCTGGATTGACATGACATGAAGCAAC 9004
661 AGGCTGTGAGAGTTCTGGGACTAAGCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 720
9005 AGGCTGTGAGAGTTCTGGGACTAAGCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 9064
721 GAATATCTCTGGCCACGAGACTATCTCTCACCCTATCCCTTTATTTCTGTTGTTCA 780
9065 GAATATCTCTGGCCACGAGACTATCTCTCACCCTATCCCTTTATTTCTGTTGTTCA 9124
781 ACAGAAGGATATTTCAGTGCACATCTGGAAACAGGATCAGTGAAGCACTGCGAGGAGTCAG 840
9125 ACAGAAGGATATTTCAGTGCACATCTGGAAACAGGATCAGTGAAGCACTGCGAGGAGTCAG 9184
841 GACTGTAGTACAGTACCATGATTTATCTATCATTCATCCACCAACATCTGTTGAGCAAG 900
9185 GACTGTAGTACAGTACCATGATTTATCTATCAATGACCAACATCTGTTGAGCAAG 9244
901 CGTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCAGAT 960
9245 CGTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCAGAT 9304
961 AGAGAGGAGCTAGTATTATAGCAGAACAGTGAACATGAC 1001
9305 AGGAGAGGAGCTAGTATTATAGCAGAACAGTGAACATGAC 9345

RESULT 4
AAA34823
ID AAA34823 standard; DNA; 9721 BP.
XX
AC AAA34823;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2512.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antispasmodic; cytoskeletal; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 673-675; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 3; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCGAAGGG 60
DB 8345 GCTTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCGAAGGG 8404

QY 61 AACGAAGGTTTTAGTAGCGGTATAGCTGAGCTTCCTGTTGTCTACCAATGCC 120
DB 8405 AACGAAGGTTTTAGTAGCGGTATAGCTGAGCTTCCTGTTGTCTACCAATGCC 8464

QY 121 CAATGCTGCTGTAGGCTAGTGTCTGTAAGAGATCTCTGTCCATCAGCCAGGACAGTCAG 180
DB 8465 CAATGCTGCTGTAGGCTAGTGTCTGTAAGAGATCTCTGTCCATCAGCCAGGACAGTCAG 8524

QY 181 CTCTCTCTTTCAGGGCAATCCCGACGCTTTTGTGAGCCAGGCTCTCTCACTCTC 240
DB 8525 CTCTCTCTTTCAGGGCAATCCCGACGCTTTTGTGAGCCAGGCTCTCTCACTCTC 8584

QY 241 CTACTCACTTAAGCCCGCTGACAGAAACACGCGCCACATTTGGTCTAAGAAACCCCTC 300
DB 8585 CTACTCACTTAAGCCCGCTGACAGAAACACGCGCGCACATTTGGTCTAAGAAACCCCTC 8644

QY 301 TGTCAATTCGCTCCACATTCGTATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
DB 8645 TGTCAATTCGCTCCACATTCGTATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704

QY 361 GTTGTGTTTTCGATTCATTGGTCTAATTTATTCAAGGGGGGCAAGTAGCAGTCTGTGA 420
DB 8705 GTTGTGTTTTCGATTCATTGGTCTAATTTATTCAAGGGGGGCAAGTAGCAGTCTGTGA 8764

QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGAGTGGTGTCTCTTTT 480
DB 8765 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGAGTGGTGTCTCTTTT 8824

QY 481 AAATCAAGTCTTTAATATACAGTGAATAATATATAGCTCAGATTTAATTAATGGGAATA 540
DB 8825 AAATCAAGTCTTTAATATACAGTGAATAATATATAGCTCAGATTTAATTAATGGGAATA 8884

QY 541 TTTATAATGAGCAAAATATGATCTGTTCAATGGTCTGAAATAAACTTCACCTGAAGAAA 600
DB 8885 TTTATAATGAGCAAAATATGATCTGTTCAATGGTCTGAAATAAACTTCACCTGAAGAAA 8944

QY 601 AAAAAAAAAAGGGTCTCTCTCTGATCATTGACTCTCTGGATTGACACTGACAGTAAGCAAC 660
DB 8945 AAAAAAAAAAGGGTCTCTCTCTGATCATTGACTCTCTGGATTGACACTGACAGTAAGCAAC 9004

QY 661 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCCCTCAITGCTGAGTGTGCAAGTACCTA 720
DB 9005 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCCCTCAITGCTGAGTGTGCAAGTACCTA 9064

QY 721 GAATATATCTTCCGACGAGACTATCTCTCAACCATCCCTTATTTCGTTGTTCA 780
DB 9065 GAATATATCTTCCGACGAGACTATCTCTCAACCATCCCTTATTTCGTTGTTCA 9124

QY 781 ACAGAAGGATATTCACTGTCACACTCTGGAACAGGATCAGCTGAAGCACTGACGGGAGTCAG 840
DB 9125 ACAGAAGGATATTCACTGTCACACTCTGGAACAGGATCAGCTGAAGCACTGACGGGAGTCAG 9184

QY 841 GACTGTAGTACAGCTACCAATGATTTATCTATCTAATGCAACCAACATCTGTTAGCAAG 900
DB 9185 GACTGTAGTACAGCTACCAATGATTTATCTATCTAATGCAACCAACATCTGTTAGCAAG 9244

QY 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCCCTCAGAT 960
DB 9245 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCCCTCAGAT 9304

QY 961 AGGAGAGGAGCTAGTTATTAAGCAGAACAAAGTAAACATGAC 1001
DB 9305 AGGAGAGGAGCTAGTTATTAAGCAGAACAAAGTAAACATGAC 9345

RESULT 5
AAA50174
ID AAA50174 standard; DNA; 9721 BP.
XX
XX AAA50174;
XX AC AC
XX 07-NOV-2000 (first entry)
XX Human interleukin-1 beta allele 1 (+6912).
XX Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;
KW coronary artery disease; osteoporosis; nephropathy; alopecia areata;
KW Graves disease; systemic lupus erythematosus; lichen sclerosis;
KW ulcerative colitis; diabetic retinopathy; periodontal disease;
KW juvenile chronic arthritis; psoriasis; insulin dependent diabetes;
KW asthma; lung fibrosis; chronic inflammatory liver disease;
KW rheumatoid arthritis; chronic inflammatory lung disease;
KW antiinflammatory; osteopathic; dermatological; immunosuppressive;
KW antidiabetic; antithyroid; antiarthritic; antirheumatic; antiasthmatic;
KW antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH replace(8904,G)
FT /*tag= a
FT /note= "IL-1B allele 1 (+6912)"
XX
PN WO200047619-A1.
XX
XX 17-AUG-2000.
PD
XX 10-FEB-2000; 2000WO-US003443.
PF
XX 10-FEB-1999; 99US-00247874.
PR
XX (INTE-) INTERLEUKIN GENETICS INC.
PA
XX Duff GW, Di Giovine FS;
PI
XX WPI; 2000-558192/51.
DR
XX Novel methods and nucleic acids for diagnosing and treating disorders
PT associated with high levels of interleukin 1beta, especially inflammatory

PS Disclosure; Page 230-232; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

XX SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match 99.78; Score 997.8; DB 3; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGTACCCAGAGTCTCTGCTGTAATGTGGACTCAATCCCTAGGGCTGGCAAGGG 60
DB 8345 GCTGTACCCAGAGTCTCTGCTGTAATGTGGACTCAATCCCTAGGGCTGGCAAGGG 8404

QY 61 AACAGAAAGGTTTTTGGTAGTACGGCTATAGCTGAGCTTCTCTGTCTACACCAATGCC 120
DB 8405 AACAGAAAGGTTTTTGGTAGTACGGCTATAGCTGAGCTTCTCTGTCTACACCAATGCC 8464

QY 121 CAATGCTGCTGCTAGGGTAGTGTCTAGAGGATCTCTGTCATCAGCCAGGACAGTCAG 180
DB 8465 CAATGCTGCTGCTAGGGTAGTGTCTAGAGGATCTCTGTCATCAGCCAGGACAGTCAG 8524

QY 181 CTCTCTCTCTTTCAGGGCCAAATCCCGCCCTTTTGTGTAGCCAGGCTCTCTCACTCTC 240
DB 8525 CTCTCTCTCTTTCAGGGCCAAATCCCGCCCTTTTGTGTAGCCAGGCTCTCTCACTCTC 8584

QY 241 CTACTCACTTAAGCCCGCTGACAGAAACACGGCCACATTTGGTTCTAAGAAACCCCTC 300
DB 8585 CTACTCACTTAAGCCCGCTGACAGAAACACGGCCACATTTGGTTCTAAGAAACCCCTC 8644

QY 301 TGTCAATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
DB 8645 TGTCAATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704

QY 361 GTTTGTTTGTGATTCATTTGGTCTAATTTATTCAAGGGGGCAAGATGAGTGTCTGTA 420
DB 8705 GTTTGTTTGTGATTCATTTGGTCTAATTTATTCAAGGGGGCAAGATGAGTGTCTGTA 8764

QY 421 AAAGAGGCTAGTTTTTAAATAGCTATGGAATCAATTTGAGCTGTGTGCTCTCTT 480
DB 8765 AAAGAGGCTAGTTTTTAAATAGCTATGGAATCAATTTGAGCTGTGTGCTCTCTT 8824

QY 481 AATCAAGTCTCTTAAATTAACACTGAAATATATAGCTCAGATTATTAAATGGGAATA 540
DB 8825 AATCAAGTCTCTTAAATTAACACTGAAATATATAGCTCAGATTATTAAATGGGAATA 8884

QY 541 TTTATAATGAGCAATATATGATCTGTTCAATGTTTCTGAATTAACACTTCACTGAGAAA 600
DB 8885 TTTATAATGAGCAATATATGATCTGTTCAATGTTTCTGAATTAACACTTCACTGAGAAA 8944

QY 601 AAAAAAAGGGTCTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC 660
DB 8945 AAAAAAAGGGTCTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC 9004

QY 661 AGGCTGTGAGAGTCTTTGGGACTTAAGCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 720
DB 9005 AGGCTGTGAGAGTCTTTGGGACTTAAGCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 9064

QY 721 GAAATATCTTGGCCACCGAAGACTATCTCTCAACCATCCCCCTTTATTTCGTTGTTCA 780
DB 9065 GAAATATCTTGGCCACCGAAGACTATCTCTCAACCATCCCCCTTTATTTCGTTGTTCA 9124

QY 781 ACAGAAGGATATTACGTGCACATCTGGAAACAGGATCAGTGAAGCACTGCGAGGGAGTCAG 840
DB 9125 ACAGAAGGATATTACGTGCACATCTGGAAACAGGATCAGTGAAGCACTGCGAGGGAGTCAG 9184

QY 841 GACTGCTAGTACAGCTACCATGATTATCTATCAATGCACCAACACATCTGTTGAGCAAG 900
DB 9185 GACTGCTAGTACAGCTACCATGATTATCTATCAATGCACCAACACATCTGTTGAGCAAG 9244

QY 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCTCAGAT 960
DB 9245 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCTCAGAT 9304

QY 961 AGGAGAGGAGCTAGTTTATAGCAGAACAGGTAACATGAC 1001
DB 9305 AGGAGAGGAGCTAGTTTATAGCAGAACAGGTAACATGAC 9345

RESULT 7

AAC63768
ID AAC63768 standard; DNA; 9721 BP.

XX AC AAC63768;

XX DT 08-FEB-2001 (first entry)

XX DE Human IL-1B gene.

XX Human; IL-1B; interleukin-1B; cytostatic; antiinflammatory;
XX immunosuppressive; dermatological; antimicrobial; antiarthritic;
XX IL-1 receptor antagonist;
XX tumour necrosis factor alpha antagonist interstitial lung disease;
XX interstitial pneumonia; pulmonary fibrosis; rheumatoid arthritis;
XX systemic lupus erythematosus; Sjogren's syndrome; systemic sclerosis;
XX dermatomyositis; chromosome 2; ds.

XX OS Homo sapiens.

XX PN WO2000060117-A2.

XX PD 12-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US008492.

XX PR 02-APR-1999; 99US-00286108.

XX PA (INTE-) INTERLEUKIN GENETICS INC.

XX PI Duff GW, Di Giovine FS, Whyte M;

XX PP WPI; 2000-656234/63.

XX PT Method for predicting the risk of interstitial lung disease, comprising
XX detecting an interleukin-1 receptor antagonist allele and tumor necrosis
XX alpha allele or an allele in linkage disequilibrium with either of these
XX alleles.

Claim 6; Fig 2; 102pp; English.

The present sequence is provided in a specification relating to a method for determining whether a subject has or is predisposed to develop an interstitial lung disease. The method involves detecting an interleukin-1 receptor antagonist (IL-1RN) (+2018) allele 2, a tumour necrosis alpha (TNF- α) (-308) allele 2, or an allele in linkage disequilibrium with either of these two alleles. The method may be used to determine whether a subject has or is predisposed to develop an interstitial pneumonia or a pulmonary fibrosis and other disorders such as rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, systemic sclerosis, dermatomyositis. The method is also used for identifying molecules which can be used as therapeutics for treating interstitial lung disease

Sequence 9721 BP: 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

```
Query Match          99.7%; Score 997.8; DB 3; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 998; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

1 GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 60

8245 CCTCTACCCACGACCTCCTGCTGCAATCTGCAATCCCTACGGCTGGAGAAAGG 8404

67 AACAGAAAGGTTTTTGTGAGTACGGCTATAGCCTGGACTTTCCTGTGTCTACACCAATGCC 120

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[illegible]

QY 421 ATAGAGCCTAGT TTTATATAGCTATGGAA TCAATTCATTTGGAC TGGTGCCTCTTT 480

DD 8703 AAAGAGCCTAGTIIITATATAGCTATGGATACAAATCCAAATTCGGACTCGTCCTCTTTT 8825

QY 481 AAATCAAGTCTTTAAATTAAACACTGAAATAATAAAGCTCAGATTAATTTAAATGGGAATA 540

DB 8825 AAATCGAGTCCCTTTAAATTAAAGACTGAAATAATATAAGCTCAGATTATTAAATGGGAAATA 8884

QY 541 TTTATAAATGAGCAAATATGATACTGTTCAATGGTTCCTGAAATAAACTTCACCTGAAGAAA 600

Db 8885 TTTATAAATGAGCAAATATCATCTACTGTTCAATGGTTCTGAAATAAACTTCACCTGAAGAAA 8944

QY
601 AAAAAAAAAAGGGTCTCTCCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAC 660

Db 8945 AAAAAAAAAAGGGTCCTCTCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAC 9004

Qy 661 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATCTGAGTGCTGCAAGTACCTA 720

Db 9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 9064

QY 721 GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCCTTATTTCGTTGTCA 780

Db 9065 GAAATATCTTGGCCACCGAAGACTATCTCTCCTCACCCATCCCCCTTATTTCGTTGTCA 9124


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Qy 1 GCTGTACCCAGAGTCTCTGTGTAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 60
Db GCTGTACCCAGAGTCTCTGTGTAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 8404
Qy 61 AACAGAAAGGTTTTAGTAGCGGTATAGCTGAGCTTTCTCTGTGTCTACACCAATGCC 120
Db AACAGAAAGGTTTTAGTAGCGGTATAGCTGAGCTTTCTCTGTGTCTACACCAATGCC 8464
Qy 121 CAACTGCTGCTTCTAGGCTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db CAACTGCTGCTTCTAGGCTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 8524
Qy 181 CTCTCTCTCTCAGGGCCCAATCCAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 240
Db CTCTCTCTCTCAGGGCCCAATCCAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 8584
Qy 241 CTACTCACTTAAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTAAGAAACCCCTC 300
Db CTACTCACTTAAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTAAGAAACCCCTC 8644
Qy 301 TGTCAATCGCTCCACATCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db TGTCAATCGCTCCACATCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704
Qy 361 GTTTGTTTGTATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 420
Db GTTTGTTTGTATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 8764
Qy 421 AAAGAGCTAGTTTTTAATAGCTATGGAATCAATTCGAATTTGGACTGGTGTCTCTTT 480
Db AAAGAGCTAGTTTTTAATAGCTATGGAATCAATTCGAATTTGGACTGGTGTCTCTTT 8824
Qy 481 AAATCAAGTCTTTAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGATA 540
Db AAATCAAGTCTTTAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGATA 8884
Qy 541 TTTTAATAGCAAAATATGATCTGTTCATGTCTGAAATAAACTTCACTGAAGAAA 600
Db TTTTAATAGCAAAATATGATCTGTTCATGTCTGAAATAAACTTCACTGAAGAAA 8944
Qy 601 AAAAAAAGGGTCTCTCTGATCATTGACTGTCTGGAATGACACTGACAGTAAGCAAC 660
Db AAAAAAAGGGTCTCTCTGATCATTGACTGTCTGGAATGACACTGACAGTAAGCAAC 9004
Qy 661 AGGCTGTGAGAGTTCTTGGGACTAAGCCACTCTCTCATTTGTGAGTGTCTGCAAGTACTA 720
Db AGGCTGTGAGAGTTCTTGGGACTAAGCCACTCTCTCATTTGTGAGTGTCTGCAAGTACTA 9064
Qy 721 GAAATATCCTTTGGCCACGAGACTATCTCTCTCAACCATCCCTTTATTGTTGTTCA 780
Db GAAATATCCTTTGGCCACGAGACTATCTCTCTCAACCATCCCTTTATTGTTGTTCA 9124
Qy 781 ACAGAGGATATTGAGTGCATCTGGAACAGGATCAGCTGAAGCACTGCGAGGAGTCAG 840
Db ACAGAGGATATTGAGTGCATCTGGAACAGGATCAGCTGAAGCACTGCGAGGAGTCAG 9184
Qy 841 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCAACCAACATCTGTTGAGCAAG 900
Db GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCAACCAACATCTGTTGAGCAAG 9244
Qy 901 CGCTATGTACTAGAGCTGGAGTACAGAGATGAGACAGTCAAGTCCCTCCTCAGAT 960
Db CGCTATGTACTAGAGCTGGAGTACAGAGATGAGACAGTCAAGTCCCTCCTCAGAT 9304
Qy 961 AGGAGAGCAGCTAGTTTATAAGCAGAACAGAGTAACATGAC 1001
Db AGGAGAGCAGCTAGTTTATAAGCAGAACAGAGTAACATGAC 9345
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RESULT 9
AAD35192
ID AAD35192 standard; DNA; 9721 Bp.

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XX AAD35192;
XX 25-JUL-2002 (first entry)
XX Human prointerleukin-1 beta (IL-1 beta) gene.
XX DE Unexplained recurrent pregnancy loss; immunologic reproductive failure;
XX KW URPL; prointerleukin-1beta; IL-1beta; human; ds.
XX OS Homo sapiens.
XX PN WO200222877-A2.
XX PD 21-MAR-2002.
XX PF 12-SEP-2001; 2001WO-US028465.
XX PR 12-SEP-2000; 2000US-0231785P.
XX PA (BGM ) BRIGHAM & WOMENS HOSPITAL INC.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Hill JA, Wang ZC, Anderson DJ, Yunis EJ;
XX WPI; 2002-362362/39.
XX DR Evaluating risk of unexplained recurrent pregnancy loss in a subject, by
XX PT testing presence of a variant in interleukin-1 beta promoter region
XX PT and/or in CD46 gene intron 1 region in a sample obtained from the
XX PT subject.
XX PS Example 2 and 3; Page 51-54; 57pp; English.
XX CC The invention relates to a method for evaluating and treating risk of
XX CC unexplained recurrent pregnancy loss (URPL) in a subject suspected of
XX CC having immunologic reproductive failure. The method involves testing a
XX CC sample obtained from the subject for the presence of a variant in the
XX CC human interleukin-1beta (IL-1beta) promoter region, and/or a variant in
XX CC the CD46 gene intron 1 region, where the presence of the variant,
XX CC indicates an elevated risk of developing recurrent pregnancy loss. The
XX CC present sequence is human prointerleukin-1 beta (IL-1 beta) gene.
XX SQ Sequence 9721 Bp; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;
Qy Query Match 99.7%; Score 997.8; DB 6; Length 9721;
Db Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Qy Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGAGCTCAATCCCTAGGGCTGGCAGAAAGG 60
8345 GCTGTACCCAGAGTCTCTGTGCTGAATGTGAGCTCAATCCCTAGGGCTGGCAGAAAGG 8404
Qy 61 AACAGAAAGGTTTTAGTAGCGGTATAGCTGAGCTTTCTCTGTGTCTACACCAATGCC 120
Db AACAGAAAGGTTTTAGTAGCGGTATAGCTGAGCTTTCTCTGTGTCTACACCAATGCC 8464
Qy 121 CAACTGCTGCTTCTAGGCTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db CAACTGCTGCTTCTAGGCTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 8524
Qy 181 CTCTCTCTCTCAGGGCCCAATCCAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 240
Db CTCTCTCTCTCAGGGCCCAATCCAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 8584
Qy 241 CTACTCACTTAAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTAAGAAACCCCTC 300
Db CTACTCACTTAAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTAAGAAACCCCTC 8644
Qy 301 TGTCAATCGCTCCACATCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db TGTCAATCGCTCCACATCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704
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361 GTTCTTTTGTATTCATTTGCTCTAAATTTATCAAGGGGGCAAGAGTAGCAGTGTCTGTGA 420
Db 8705 GTTCTTTTGTATTCATTTGCTCTAAATTTATCAAGGGGGCAAGAGTAGCAGTGTCTGTGA 8764

421 AAAGAGCCTAGTTTATATAGCTATGGAATCAATTCATTTGGAGCTGGTGTCTCTTT 480
Db 8765 AAAGAGCCTAGTTTATATAGCTATGGAATCAATTCATTTGGAGCTGGTGTCTCTTT 8824

481 AAATCAAGTCCTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAATGGGAATA 540
Db 8825 AAATCAAGTCCTTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTAATGGGAATA 8884

541 TTATTAATAGCAATATGATGATGTTCAATGGTTCTGAATAAATCACTCACTGAAGAAA 600
Db 8885 TTATTAATAGCAATATGATGATGTTCAATGGTTCTGAATAAATCACTCACTGAAGAAA 8944

601 AAAAAAAGAGGTCTCTCTGATCATTCAGCTGCTGGAATTCACACTGACAGTAGCAAC 660
Db 8945 AAAAAAAGAGGTCTCTCTGATCATTCAGCTGCTGGAATTCACACTGACAGTAGCAAC 9004

661 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCTGAGTGTGCAAGTACCTA 720
Db 9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCTGAGTGTGCAAGTACCTA 9064

721 GAAATATCTTTGGCCACGGAAGACTATCTCTCAACCATCCCTTTATTCGTGTCTCA 780
Db 9065 GAAATATCTTTGGCCACGGAAGACTATCTCTCAACCATCCCTTTATTCGTGTCTCA 9124

781 ACAGAAGGATATTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 840
Db 9125 ACAGAAGGATATTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 9184

841 GACTGGTAGTAACAGCTACCAATGATTTATCTATCAATGACCAACATCTGTTGAGCAAG 900
Db 9185 GACTGGTAGTAACAGCTACCAATGATTTATCTATCAATGACCAACATCTGTTGAGCAAG 9244

901 CGCTATGTAAGAGCTGGGAGTACAGAGATGAGAACAGTCACAGTCCCTCTCTCAGAT 960
Db 9245 CGCTATGTAAGAGCTGGGAGTACAGAGATGAGAACAGTCACAGTCCCTCTCTCAGAT 9304

961 AGGAGAGCAGCTAGTTATAGCAAGAACAGGTAACATGAC 1001
Db 9305 AGGAGAGCAGCTAGTTATAGCAAGAACAGGTAACATGAC 9345

RESULT 10
ID ABZ96639 standard; DNA; 9721 BP.
XX AC ABZ96639;
XX DT 17-OCT-2003 (first entry)
XX DE Human interleukin-1 nucleic acid.
XX KW Human; antitense; lung dysfunction; nasal airway dysfunction;
KW antinflammatory steroid; ubiquinone; antinflammatory; antiallergic;
KW antiallergic; hypotensive; immunosuppressive; cytosolic; gene therapy;
KW antitense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmacological composition for treating ailments associated with impaired
PT respiration, has oligo(s) antitense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 11881; 872pp; English.
XX PS The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antitense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antinflammatory steroid and ubiquinone. A composition of the invention
CC has antinflammatory, antiallergic, antialsthatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antitense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;
Query Match 99.7%; Score 997.8; DB 7; Length 9721;
Best Local Similarity 99.8%; Pred No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGTACCCAGAGTCTCTGTCTGCTGAATGTGAGTCAATTCCTAGGCTGCAGAAAGG 60
Db 8345 GCTGTACCCAGAGTCTCTGTCTGCTGAATGTGAGTCAATTCCTAGGCTGCAGAAAGG 8404

61 AACAGAAAGGTTTTGAGTACGGCTATAGCTGGAGTTTCTGTGTGTCTACCAATGCC 120
Db 8405 AACAGAAAGGTTTTGAGTACGGCTATAGCTGGAGTTTCTGTGTGTCTACCAATGCC 8464

121 CAATGCTCTGCTTAGGGTAGTGTCTTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db 8465 CAATGCTCTGCTTAGGGTAGTGTCTTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 8524

181 CTCTCTCTTTTTCAGGGCAATCCCGAGCCCTTTTGTGAGCCAGCCCTCTCTCACTCTC 240
Db 8525 CTCTCTCTTTTTCAGGGCAATCCCGAGCCCTTTTGTGAGCCAGCCCTCTCTCACTCTC 8584

241 CTACTCACTTAAAGCCCGCTGCACAGAAACCAAGCCCATTTGGTGTCTAAGAAACCCCTC 300
Db 8585 CTACTCACTTAAAGCCCGCTGCACAGAAACCAAGCCCATTTGGTGTCTAAGAAACCCCTC 8644

301 TGTCTATGCTCCCACTCTGTATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT 360
Db 8645 TGTCTATGCTCCCACTCTGTATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT 8704

361 GTTCTGTTTGTATTCATTTGCTCTAAATTTATCAAGGGGGCAAGAGTAGCAGTGTCTGTA 420
Db 8705 GTTCTGTTTGTATTCATTTGCTCTAAATTTATCAAGGGGGCAAGAGTAGCAGTGTCTGTA 8764

421 AAAGAGCCTAGTTTATATAGCTATGGAATCAATTCATTTGGAGCTGGTGTCTCTTT 480
Db 8765 AAAGAGCCTAGTTTATATAGCTATGGAATCAATTCATTTGGAGCTGGTGTCTCTTT 8824

481 AAATCAAGTCCTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAATGGGAATA 540

Db 8825 AAATCAAGTCTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 8884
Qy 541 TTTATAATGAGCAAAATATGATATCTGTTCAATGGTCTGAAATATAAACTTCACTGAAGAAA 600
Db 8885 TTTATAATGAGCAAAATATCATACTGTTCAATGGTCTGAAATATAAACTTCACTGAAGAAA 8944
Qy 601 AAAAAAAGGGTCTCTCCCTGATCATATGATGCTGTTGATGATGACACTGACAGTAAGCAAC 660
Db 8945 AAAAAAAGGGTCTCTCCCTGATCATATGATGCTGTTGATGATGACACTGACAGTAAGCAAC 9004
Qy 661 AGGCTGAGAGTCTCTGGGACTAAGCCCACTCTCATCTGCTGAGTGTCTCAAGTACCTA 720
Db 9005 AGGCTGAGAGTCTCTGGGACTAAGCCCACTCTCATCTGCTGAGTGTCTCAAGTACCTA 9064
Qy 721 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCCATCTTATTTGTTGTTCA 780
Db 9065 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCCATCTTATTTGTTGTTCA 9124
Qy 781 ACAGAGGATATTCAGTGACATCTGGAACAGGATCAGCTGAAGCACTGCAGGAGTTCAG 840
Db 9125 ACAGAGGATATTCAGTGACATCTGGAACAGGATCAGCTGAAGCACTGCAGGAGTTCAG 9184
Qy 841 GACTGGTAGTACAGCTACCATGATTTATCTATCAATGCAACCAACATCTGTTGAGCAAG 900
Db 9185 GACTGGTAGTACAGCTACCATGATTTATCTATCAATGCAACCAACATCTGTTGAGCAAG 9244
Qy 901 CGCTATCTAGAGCTGGAGTACAGATGAGACAGTCAAGTCAAGTCCCTCTCAGAT 960
Db 9245 CGCTATCTAGAGCTGGAGTACAGATGAGACAGTCAAGTCAAGTCCCTCTCAGAT 9304
Qy 961 AGGAGGCGAGTCTGTTATTAAGCAGAAACAAGGTAACATGAC 1001
Db 9305 AGGAGGCGAGTCTGTTATTAAGCAGAAACAAGGTAACATGAC 9345

RESULT 11
AAD51464
ID AAD51464 standard; DNA; 9721 BP.
XX AC AAD51464;
XX DT 16-APR-2003 (first entry)
XX DE Human interleukin-1B (IL-1B) gene.
XX KW Drug screening; fungicide; gene therapy; antibacterial; infection;
XX KW virucide; human; interleukin-1; IL-1; gene; ds.
XX OS Homo sapiens.
XX FN WO2002101015-A2.
XX PD 19-DEC-2002.
XX PF 11-JUN-2002; 2002WO-US018346.
XX PR 11-JUN-2001; 2001US-0297305P.
XX PA (INTE-) INTERLEUKIN GENETICS INC.
XX PI Dower S, Duff GW;
XX WP1; 2003-148793/14.
XX DR
XX PT New detection reagent, useful for monitoring molecular assembly events to
XX PT permit the dissection of genetic and non-genetic influences on biological
XX PT activity, comprises an interactive sensor pair.
XX PS Disclosure; Fig 3; 56pp; English.
XX CC The invention relates to methods, compositions and apparatus for
XX CC monitoring molecular assembly events. It also relates to a detection

CC reagent comprising an interactive sensor pair. The detection reagent is
CC useful for monitoring molecular assembly events to permit the dissection
CC of genetic and non-genetic influences on a particular biological
CC activity. The method is useful for linking genetic variations to
CC molecular and physiological events, drug screening, diagnostics, therapy
CC selection and dosing, patient monitoring or environmental safety. The
CC interactive sensor pairs may be used to screen for and identify novel
CC agonists and antagonists or other molecules that modulate a biological
CC activity. The method is also useful for selecting an appropriate targeted
CC therapeutic for a subject having an infection, including viral, bacterial
CC or fungal infection. It is also used in gene therapy. The present
CC sequence is human interleukin-1 (IL-1) allelic gene. This sequence is
XX used to illustrate the method of the invention
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;
Query Match 99.7%; Score 997.8; DB 7; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCTGTACCCAGAGAGTCTGTGCTGAATGTGACATCAATCCTAGGGCTGGCAGAAAGG 60
Db 8345 GCTGTACCCAGAGAGTCTGTGCTGAATGTGACATCAATCCTAGGGCTGGCAGAAAGG 8404
Qy 61 AACAGAAAAGTTTTTGGTACGGCTATAGCCTGGACTTTCCCTGTTGTCTACACCAATGCC 120
Db 8405 AACAGAAAAGTTTTTGGTACGGCTATAGCCTGGACTTTCCCTGTTGTCTACACCAATGCC 8464
Qy 121 CAACTGCCTGCTTAGGTAGTGTCTAAGGAGTCTCCTGTCATCAGCCAGCAGACAGTCTCAG 180
Db 8465 CAACTGCCTGCTTAGGTAGTGTCTAAGGAGTCTCCTGTCATCAGCCAGCAGACAGTCTCAG 8524
Qy 181 CTCTCTCTCTTTCAGGGCCAAATCCCCAGGCCCTTTTGTGAGCCAGGCCCTCTCTCAGCTCTC 240
Db 8525 CTCTCTCTTTCAGGGCCAAATCCCCAGGCCCTTTTGTGAGCCAGGCCCTCTCTCAGCTCTC 8594
Qy 241 CTACTCATTAAAGCCCGCTGACAGAAACACAGGCCACATTTGGTTCTTAAGAAACCCCTC 300
Db 8585 CTACTCATTAAAGCCCGCTGACAGAAACACAGGCCACATTTGGTTCTTAAGAAACCCCTC 8644
Qy 301 TGTCTATGCTCCCACTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTATTGTTT 360
Db 8645 TGTCTATGCTCCCACTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTATTGTTT 8704
Qy 361 GTTGTCTTTGATTCATTGGTCTTAATTTATTCAAAGGGGGCAAGAGTACAGTCTCTGTA 420
Db 8705 GTTGTCTTTGATTCATTGGTCTTAATTTATTCAAAGGGGGCAAGAGTACAGTCTCTGTA 8764
Qy 421 AAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTCTCTCTTT 480
Db 8765 AAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTCTCTCTTT 8824
Qy 481 AAATCAAGTCTTTTAATTAACACTGAAATATATTAAGCTCAGATTATTATTAATGGGAATA 540
Db 8825 AAATCAAGTCTTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTATTAATGGGAATA 8884
Qy 541 TTTATAATGAGCAAAATATGATATCTGTTCAATGGTCTGAAATATAAACTTCACTGAAGAAA 600
Db 8885 TTTATAATGAGCAAAATATCATACTGTTCAATGGTCTGAAATATAAACTTCACTGAAGAAA 8944
Qy 601 AAAAAAAGGGTCTCTCTCTGATCATATGCTGTCTGGATTGACACTGACAGTAAGCAAC 660
Db 8945 AAAAAAAGGGTCTCTCTCTGATCATATGCTGTCTGGATTGACACTGACAGTAAGCAAC 9004
Qy 661 AGGCTGTGAGATCTTGGGACTAAGCCCACTCTCCCTCATCTGCTGAGTGTCTGCAAGTACCTA 720
Db 9005 AGGCTGTGAGATCTTGGGACTAAGCCCACTCTCCCTCATCTGCTGAGTGTCTGCAAGTACCTA 9064
Qy 721 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCCATCTTATTTGTTGTTCA 780
Db 9065 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCCATCTTATTTGTTGTTCA 9124
Qy 781 ACAGAGGATATTCAGTGACATCTGGAACAGGATCAGCTGAAGCACTGCAGGAGTTCAG 840

Db 9125 ACAGAAGGATATTCAGTGCACATCTGGAAACAGGATCAGTGAAGCACTGCGAGGAGTCAG 9184
QY 841 GACTGGTAGTAACAGCTACCATGATTTATCTATCATGACCAACATCTGTTGAGCAAG 900
Db 9185 GACTGGTAGTAACAGCTACCATGATTTATCTATCATGACCAACATCTGTTGAGCAAG 9244
QY 901 CCGTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGATGCCCTCTCAGAT 960
Db 9245 CCGTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGATGCCCTCTCAGAT 9304
QY 961 AGGAGAGGAGCTAGTTATTAAGCAGAACAAAGGTAAACATGAC 1001
Db 9305 AGGAGAGGAGCTAGTTATTAAGCAGAACAAAGGTAAACATGAC 9345

RESULT 12

AA154516
ID AA154516 standard; DNA; 9721 BP.

XX AC AA154516;

DT 16-APR-2003 (first entry)

XX Interleukin-1B nucleotide sequence.

KW Early onset; progression; ageing-related condition; BOA; allele;
KW interleukin; (IL)-1; pattern 1; pattern 2; pattern 3; osteoporosis;
KW osteoarthritis; wrinkled skin; age-related cancer; lifestyle; exercise;
KW diet; nutraceutical; ds.

XX Unidentified.

OS WO2002103031-A2.

XX 27-DEC-2002.

PF 17-JUN-2002; 2002WO-US019205.

XX 15-JUN-2001; 2001US-0298493P.

XX (INTE-) INTERLEUKIN GENETICS INC.

PI Barnett K, Crossman DC, Duff GW, Francis SE, Kornman KS;

XX WPI; 2003-167530/16.

PT Determining a subject's susceptibility to an early onset or progression
PT of an ageing-related condition, useful for customizing therapy, comprises
PT detecting the presence of an allele of an interleukin-1 pattern 1,
PT pattern 2 and/or pattern 3.

PS Disclosure; Fig 5; 98pp; English.

CC The invention relates to a novel method for determining a subject's
CC susceptibility to the early onset or progression of an ageing-related
CC condition (EOA). The novel method comprises assessing the subject's
CC genotype with respect to at least one allele of an interleukin (IL)-1
CC pattern 1, pattern 2 and/or pattern 3 (the presence or absence of at
CC least 1 allele provides information about the subject's susceptibility to
CC an early onset or progression of an ageing-related condition). The method
CC is useful for determining or predicting a subject's susceptibility to the
CC early onset or progression of an ageing-related condition (e.g.
CC osteoporosis, osteoarthritis, wrinkled skin, or age-related cancer) and
CC for determining an ageing-related phenotype. The method may be a
CC customised therapy based on the individual's genetic profile, to tailor a
CC recommended lifestyle, including changes in exercise and diet, and to
CC recommend nutraceuticals that are predicted to benefit a subject having a
CC particular IL-1 genotype and BOA predisposition. This polynucleotide
CC sequence represents an interleukin nucleotide sequence relating to the
CC invention

XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 7; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7,8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGTACCCAGAGAGTCTGTCTGTAATGTGGAATCAATCCCTAGGGCTGGCAGAAAGGG 60
Db 8345 GCTGTACCCAGAGAGTCTGTCTGTAATGTGGAATCAATCCCTAGGGCTGGCAGAAAGGG 8404
QY 61 AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACCAATGCC 120
Db 8405 AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACCAATGCC 8464
QY 121 CAACTGCCTTGGCTTAGGGTAGTGCCTAAAGAGGATCTCCTGTCCATCAGCCAGCAGTGCAG 180
Db 8465 CAACTGCCTTGGCTTAGGGTAGTGCCTAAAGAGGATCTCCTGTCCATCAGCCAGCAGTGCAG 8524
QY 181 CTCTCTCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGGCCAGGCTCTCTCAGCTCTC 240
Db 8525 CTCTCTCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGGCCAGGCTCTCTCAGCTCTC 8584
QY 241 CTACTCAGTTAAAGCCCGCTGACAGAAACACACGGCCACATTTGGTCTTAAGAAACCCCTC 300
Db 8585 CTACTCAGTTAAAGCCCGCTGACAGAAACACACGGCCACATTTGGTCTTAAGAAACCCCTC 8644
QY 301 TGTCAATCGCTCCCAATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT 360
Db 8645 TGTCAATCGCTCCCAATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT 8704
QY 361 GTTTGTTTTGATTCATTTGGTCTTAATTTTCAAGGGGGCAAGTAGTACGAGTGTCTGA 420
Db 8705 GTTTGTTTTGATTCATTTGGTCTTAATTTTCAAGGGGGCAAGTAGTACGAGTGTCTGA 8764
QY 421 AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTCTCTCTTT 480
Db 8765 AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTCTCTCTTT 8824
QY 481 AAATCAAGTCCCTTTAATTAACACTGAAATATATTAAGCTCAGATTTATTTAAATGGGAATA 540
Db 8825 AAATCAAGTCCCTTTAATTAAGACTGAAATATATTAAGCTCAGATTTATTTAAATGGGAATA 8884
QY 541 TTTTAAATGAGCAAAATATGATATCTGTTCAATGGTCTCAATTAATAAATCACTCAAGAAA 600
Db 8885 TTTTAAATGAGCAAAATATGATATCTGTTCAATGGTCTCAATTAATAAATCACTCAAGAAA 8944
QY 601 AAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTGAAGCAAAAC 660
Db 8945 AAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTGAAGCAAAAC 9004
QY 661 AGGCTGTGAGAGTCTCTGGGACTAAGCCCACTCCCTCATTTGCTGAGTGTGCAAGTACCTA 720
Db 9005 AGGCTGTGAGAGTCTCTGGGACTAAGCCCACTCCCTCATTTGCTGAGTGTGCAAGTACCTA 9064
QY 721 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCATCCCTTTATTTGTTGTTCA 780
Db 9065 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCATCCCTTTATTTGTTGTTCA 9124
QY 781 ACAGAGGATATTTAGTGCACATCTGGAAACAGGATCAGCTGAAGCACTGCGAGGAGTGCAG 840
Db 9125 ACAGAGGATATTTAGTGCACATCTGGAAACAGGATCAGCTGAAGCACTGCGAGGAGTGCAG 9184
QY 841 GACTGGTAGTAACAGCTACCATGATTTTATCTATCAATGACCAAAACATCTGTTGAGCAAG 900
Db 9185 GACTGGTAGTAACAGCTACCATGATTTTATCTATCAATGACCAAAACATCTGTTGAGCAAG 9244
QY 901 CCGTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCAGAT 960
Db 9245 CCGTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCAGAT 9304
QY 961 AGGAGAGGAGCTAGTTATTAAGCAGAACAAAGGTAAACATGAC 1001
Db 9305 AGGAGAGGAGCTAGTTATTAAGCAGAACAAAGGTAAACATGAC 9345

RESULT 13		Best Local Similarity 99.8%; Pred. No. 9e-235;		Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
ACC83528	ACC83528	standard; DNA; 15402 BP.			
XX	XX				
AC	AC				
XX	XX				
DT	DT	08-SEP-2003 (first entry)			
XX	XX				
DE	DE	Human interleukin-1 beta gene.			
XX	XX				
KW	KW	Interleukin-1 beta; IL-1B; human; single nucleotide polymorphism; SNP;			
KW	KW	antiinflammatory; noctropic; antirheumatic; antiarthritic; cardiant;			
KW	KW	antilucer; ophthalmological; anidiabetic; lipolytic; antiasthmatic;			
XX	XX	gene; ds.			
XX	XX				
OS	OS	Homo sapiens.			
XX	XX				
FH	FH	Key Location/Qualifiers			
FT	FT	variation replace(3870,t)			
FT	FT	/*tag= a			
FT	FT	/standard.name= "Single nucleotide polymorphism"			
FT	FT	/note= "-3737 polymorphic allele 1"			
XX	XX				
PN	PN	W02003044176-A2.			
XX	XX				
PD	PD	30-MAY-2003.			
XX	XX				
XX	XX	19-NOV-2002; 2002WO-US037222.			
PF	PF				
XX	XX				
PR	PR	19-NOV-2001; 2001US-0331681P.			
PR	PR	05-JUN-2002; 2002US-0386020P.			
XX	XX				
PA	PA	(INTE-) INTERLEUKIN GENETICS INC.			
XX	XX				
PI	PI	Wyllie D, Duff GW, Aziz N, Hsieh CM;			
XX	XX				
DR	DR	WPI; 2003-457608/43.			
XX	XX				
PT	PT	New nucleic acid, useful for preparing a composition for treating an			
PT	PT	inflammatory disease or condition associated with increased interleukin			
PT	PT	production in a human subject, e.g. rheumatoid arthritis or ulcerative			
PT	PT	colitis.			
XX	XX				
PS	PS	Disclosure; Fig 1; 107pp; English.			
XX	XX				
CC	CC	The present sequence is that of the interleukin-1 beta (IL-1B) gene			
CC	CC	including the upstream promoter region. A novel function-altering			
CC	CC	polymorphism has been discovered at position -3737 in the distal upstream			
CC	CC	promoter region. The IL-1B (-3737) type 1 allele (C) is associated with			
CC	CC	increased IL-1B expression and is associated with inflammatory disease. A			
CC	CC	claimed method of diagnosing an increased likelihood of developing an			
CC	CC	inflammatory disease or condition associated with increased interleukin			
CC	CC	production in a subject involves determining the identity of the -3737 IL			
CC	CC	-1B allele as a type 1 (C) or type 2 (T) promoter sequence. The			
CC	CC	inflammatory disease is especially a periodontal disease or Alzheimer's			
CC	CC	disease, or is amyotrophic lateral sclerosis, arthritis, collagen-induced			
CC	CC	arthritis, juvenile chronic arthritis, juvenile rheumatoid arthritis,			
CC	CC	osteoarthritis, asthma, cardiovascular disease, autoimmune diabetes,			
CC	CC	insulin-dependent diabetes, diabetic periodontitis, diabetic retinopathy,			
CC	CC	diabetic nephropathy, coeliac disease, chronic colitis, Crohn's disease,			
CC	CC	inflammatory bowel disease, ulcerative colitis, gastric ulcer, hepatic			
CC	CC	inflammation, cholesterol gallstones, hepatic fibrosis, Kawasaki's			
CC	CC	syndrome, multiple sclerosis, nephropathy, neurodegenerative disease,			
CC	CC	ophthalmopathy, pancreatic acinosis, pulmonary disease, restenosis,			
CC	CC	rheumatoid arthritis, thyroiditis, alopecia areata, autoimmune			
CC	CC	myocarditis and Graves' disease (all claimed). Determining the identity			
CC	CC	of the -3737 IL-1B allele is also useful for determining whether a			
CC	CC	subject can be effectively treated with a therapeutic drug			
XX	XX				
SQ	SQ	Sequence 15402 BP; 4453 A; 3490 C; 3462 G; 3995 T; 0 U; 2 Other;			

Query Match

99.7%; Score 997.8; DB 7; Length 15402;

RESULT 14

AAA34828
ID AAA34828 standard; DNA; 29433 BP.
AC AAA34828;
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2517.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US017712.
XX
XX 03-AUG-1998; 98US-0095212P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
XX Disclosure; Page 677-684; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
XX Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 0 U; 2 Other;
Query Match 99.7%; Score 997.8; DB 3; Length 29433;
Best Local Similarity 99.8%; Pred. No. 1.1e-234;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 15

AAF20950

ID AAF20950 standard; DNA; 29433 BP.

XX

Tue Jul 6 08:49:57 2004

us-09-247-874e-2_copy_8345_9345.rng

Page 16

Job time : 467 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 10:39:01 ; Search time 2592 seconds
(without alignments)
11532.424 Million cell updates/sec

Title: US-09-247-874E-2_COPY_8345_9345

Perfect score: 1001
Sequence: 1 gctgtaccacagagatccg.....gcagaacaaggtaacatgatc 1001

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	595.4	59.5	705	13	BU626628 UI-H-FTO-
C 2	595.4	59.5	777	14	CD367424 UI-H-FT1-
C 3	593.8	59.3	618	14	CD368885 UI-H-FT1-
C 4	593.8	59.3	618	14	CD370914 UI-H-FT1-

C 5	593.8	59.3	668	14	CA431510
C 6	593.8	59.3	671	14	CA307004
C 7	593.8	59.3	701	13	BU626429
C 8	593.8	59.3	704	13	BU626613
C 9	593.8	59.3	706	13	BU626909
C 10	593.8	59.3	767	14	CA305984
C 11	593.8	59.3	767	14	CA442834
C 12	593.8	59.3	770	12	BQ000281
C 13	593.8	59.3	777	14	CA431534
C 14	593.8	59.3	798	14	CA307234
C 15	592.8	59.2	703	12	BQ001221
C 16	592.2	59.2	665	14	CD367786
C 17	592.2	59.2	704	14	CA443067
C 18	589.6	58.9	669	13	BU626499
C 19	588.4	58.8	638	13	BU626893
C 20	585.8	58.5	603	14	CD370521
C 21	579.8	57.9	793	12	BM999417
C 22	577.6	57.7	817	9	AI609005
C 23	573.8	57.3	656	14	CA310014
C 24	573.8	57.3	696	13	BU626962
C 25	567.4	56.7	619	14	CA441158
C 26	567.2	56.7	673	13	BU626793
C 27	562	56.1	618	10	AW273081
C 28	554.2	55.4	575	14	CA431636
C 29	543	54.2	749	12	EG117168
C 30	539.2	53.9	911	12	EG194765
C 31	536.8	53.6	698	9	AI471571
C 32	536	53.5	676	14	CA310223
C 33	523	52.2	548	12	BM997237
C 34	506.2	50.6	554	9	AA577318
C 35	502	50.1	521	9	AI022364
C 36	481.6	48.1	549	9	AI566931
C 37	461.8	46.1	528	9	AI678441
C 38	437.6	43.7	514	9	AA131744
C 39	430	43.0	746	12	B1519707
C 40	400	40.0	454	14	D20737
C 41	399.6	39.9	430	14	W47101
C 42	389.8	38.9	703	9	AV715551
C 43	388	38.8	413	14	W38319
C 44	384	38.4	429	14	T29172
C 45	357.6	35.7	741	14	CD639977

ALIGNMENTS

RESULT 1
BU626628/c
LOCUS
DEFINITION
UI-H-FTO-bhm-1-22-0-UI-s1 NCI CGAP FTO Homo sapiens cDNA clone
UI-H-FTO-bhm-1-22-0-UI 3', mRNA sequence.
ACCESSION
BU626628
VERSION
BU626628.1 GI:23292843
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 705)
NCI-CGAP, <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Robeff Pamela, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n\$Simple_repeat

CA431510	UI-H-FTO-
CA307004	UI-H-FT1-
BU626429	UI-H-FTO-
BU626613	UI-H-FTO-
BU626909	UI-H-FT1-
CA305984	UI-H-FTO-
CA442834	UI-H-FTO-
BQ000281	UI-H-FTO-
CA431534	UI-H-FTO-
CA307234	UI-H-FT1-
BQ001221	UI-H-FT1-
CD367786	UI-H-FT1-
CA443067	UI-H-FTO-
BU626499	UI-H-FTO-
BU626893	UI-H-FTO-
CD370521	UI-H-FT1-
BM999417	UI-H-FTO-
AI609005	tw85g07.x
CA310014	UI-H-FT1-
BU626962	UI-H-FTO-
CA441158	UI-H-FTO-
BU626793	UI-H-FTO-
AW273081	xu27h01.x
CA431636	UI-H-FTO-
EG117168	602346446
EG194765	RST14064
AI471571	cl98h09.x
CA310223	UI-H-FT1-
BM997237	UI-H-FTO-
AA577318	nm89a08.s
AI022364	ow64g05.x
AI566931	tg67h02.x
AI678441	tn92d01.x
AA131744	z135f02.s
B1519707	603061928
D20737	HUMGS01714
W47101	zc39b04.s1
AV715551	AV715551
W38319	zc77b02.s1
T29172	EST71708 Hu
CD639977	AGENCOURT

Seq primer: M13 FORWARD

POLYA=yes.

FEATURES

source

Location/Qualifiers

1..705

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="NCI CGAP FTO"

/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP_FTO is a cDNA library constructed from a pool of

81 RNA samples from Alveolar Macrophages challenged with

different treatments. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into p773-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tag for this library is GGCCATGCCG. The cell line

was provided by Gary W. Hunninghake from the University of

Iowa.

TAG_LIB=UI-H-FTO

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match

Best Local Similarity

Matches 607; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

59.5%; Score 595.4; DB 13; Length 705;

99.7%; Pred. No. 3.2e-108;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

1; Indels 1; Gaps 1;

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541 TTTTAAATGAGCAAAATATGATCTGTTCAATGTTCTGAAATAAACTTCACTGAGAAA 600

72 TTTTAAATGAGCAAAATATGATCTGTTCAATGTTCTGAAATAAACTTCACTGAGAAA 13

601 AAAAAAAAAA 609

12 AAAAAAAAAA 4

CD367424

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QY	1	GCTGTACCCAGAGAGCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	60
Db	611	GCTGTACCCAGAGAGCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	552
QY	61	AACAGAAAGGTTTGTAGTACGGCTATAGCTGGAGCTTCTCTGTGTCTACACCAATGCC	120
Db	551	AACAGAAAGGTTTGTAGTACGGCTATAGCTGGAGCTTCTCTGTGTCTACACCAATGCC	492
QY	121	CAACTGCTCCCTTAGGTAGTCTCTAGAGGATCTCTGTCCATCAGCCAGGACAGCTCAG	180
Db	491	CAACTGCTCCCTTAGGTAGTCTCTAGAGGATCTCTGTCCATCAGCCAGGACAGCTCAG	432
QY	181	CTCTCTCTTTTCAAGGCGCAATCCCGAGCTTTTGTGTAGCCAGGCTCTCTCACTCTTC	240
Db	431	CTCTCTCTTTTCAAGGCGCAATCCCGAGCTTTTGTGTAGCCAGGCTCTCTCACTCTTC	372
QY	241	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTAAGAAACCCCTC	300
Db	371	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTAAGAAACCCCTC	312
QY	301	TGTCATTCGCTCCACATTCGTATGAGCAACCCGCTTCCCTATTATTTATTTATTTT	360
Db	311	TGTCATTCGCTCCACATTCGTATGAGCAACCCGCTTCCCTATTATTTATTTATTTT	252
QY	361	GTGTGTTTGAATTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	420
Db	251	GTGTGTTTGAATTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	193
QY	421	AAAGAGCTAGTTTATTAATAGCTATGGAATCAATTTGAGCTGGTGTGCTCTCTTT	480
Db	193	AAAGAGCTAGTTTATTAATAGCTATGGAATCAATTTGAGCTGGTGTGCTCTCTTT	133
QY	481	AAATCAAGTCTTTTAAATTAACACTGAAATATATAGCTCAGATTTTAAATGGAATA	540
Db	133	AAATCAAGTCTTTTAAATTAACACTGAAATATATAGCTCAGATTTTAAATGGAATA	73
QY	541	TTTATAATGAGCAATATCATCTGTTCAATGTTCTGAATGTTCTGAATGTTCTGAAT	600
Db	73	TTTATAATGAGCAATATCATCTGTTCAATGTTCTGAATGTTCTGAATGTTCTGAAT	13
QY	601	AAAAAATAA 609	
Db	12	AAAAAATAA 4	
RESULT 3			
CD368885/c			
LOCUS			
DEFINITION	UI-H-FT1-bjx-d-03-0-UI-s1 NCI CGAP FT1 Homo sapiens cDNA clone	618 bp	linear EST 29-MAY-2003
ACCESSION	CD368885		
VERSION	CD368885.1	GI:31152975	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 618)		
JOURNAL	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaps-remail.nih.gov		
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I		
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Distribution information can be found at		
	http://genome.uiowa.edu/distribution/cgap.html		
	The following repetitive elements were found in this cDNA		
	sequence: 221-272, >(TAAA)n#Simple_repeat		
	Seq primer: M13 FORWARD		
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source			
Location/Qualifiers			
1..618			
/organism="Homo sapiens"			
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/clones="UI-H-FT1-bjx-d-03-0-UI"			
/tissue_type="Aveolar Macrophage"			
/dev_stage="Adult"			
/lab_host="DH10B (Life Technologies)"			
/clone_lib="NCI CGAP FT1"			
/note="Torgan: Lung; Vector: pT73-Pac (Pharmacia) with a			
modified polylinker; Site 1: EcoR I; Site 2: Not I;			
NCI CGAP FT1 is a normalized cDNA library constructed from			
a pool of 81 RNA samples from Alveolar Macrophages			
challenged with different treatments. The library was			
normalized according to Bonaldo, Lennon and Soares, Genome			
Research, 6:791-806, 1996. First strand cDNA synthesis was			
primed with an oligo-dT primer containing a Not I site.			
Double stranded cDNA was ligated to an EcoR I adaptor,			
digested with Not I, and cloned directionally into			
pT73-Pac vector. The oligonucleotide used to prime the			
synthesis of first-strand cDNA contains a library tag			
sequence that is located between the Not I site and the			
(dT)18 tail. The sequence tag for this library is			
GGCCATGCG. The tissue was provided by Dr. Gary W.			
Hunninghake of the University of Iowa			
hunninghake@iowa.uiowa.edu			
TAG LIB=UI-H-FT1			
TAG_SEQ=GGCCATGCG			
ORIGIN			
* Query Match	59.3%;	Score 593.8;	DB 14; Length 618;
Best Local Similarity	99.5%;	Pred. No. 7,1e-108;	
Matches	606;	Conservative 0;	Mismatches 2; Indels 1; Gaps 1;
QY	1	GCTGTACCCAGAGAGCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	60
Db	611	GCTGTACCCAGAGAGCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	552
QY	61	AACAGAAAGGTTTGTAGTACGGCTATAGCTGGAGCTTCTCTGTGTCTACACCAATGCC	120
Db	551	AACAGAAAGGTTTGTAGTACGGCTATAGCTGGAGCTTCTCTGTGTCTACACCAATGCC	492
QY	121	CAACTGCTCCCTTAGGTAGTCTCTAGAGGATCTCTGTCCATCAGCCAGGACAGCTCAG	180
Db	491	CAACTGCTCCCTTAGGTAGTCTCTAGAGGATCTCTGTCCATCAGCCAGGACAGCTCAG	432
QY	181	CTCTCTCTTTTCAAGGCGCAATCCCGAGCTTTTGTGTAGCCAGGCTCTCTCACTCTTC	240
Db	431	CTCTCTCTTTTCAAGGCGCAATCCCGAGCTTTTGTGTAGCCAGGCTCTCTCACTCTTC	372
QY	241	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTAAGAAACCCCTC	300
Db	371	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTAAGAAACCCCTC	312
QY	301	TGTCATTCGCTCCACATTCGTATGAGCAACCCGCTTCCCTATTATTTATTTATTTT	360
Db	311	TGTCATTCGCTCCACATTCGTATGAGCAACCCGCTTCCCTATTATTTATTTATTTT	252
QY	361	GTGTGTTTGAATTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	420
Db	251	GTGTGTTTGAATTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	193
QY	421	AAAGAGCTAGTTTATTAATAGCTATGGAATCAATTTGAGCTGGTGTGCTCTCTTT	480
Db	193	AAAGAGCTAGTTTATTAATAGCTATGGAATCAATTTGAGCTGGTGTGCTCTCTTT	133
QY	481	AAATCAAGTCTTTTAAATTAACACTGAAATATATAGCTCAGATTTTAAATGGAATA	540
Db	133	AAATCAAGTCTTTTAAATTAACACTGAAATATATAGCTCAGATTTTAAATGGAATA	73
QY	541	TTTATAATGAGCAATATCATCTGTTCAATGTTCTGAATGTTCTGAATGTTCTGAAT	600

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Db      72 TTTTAAATGACAAATATCATCTGTTCTGAATAAATCTACTGAAGAA 13
QY      601 AAAAAAAAA 609
Db      12 AAAAAAAAA 4

RESULT 4
CD370914/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD370914      618 bp      mRNA      linear      EST 29-MAY-2003
UI-H-Ftl-bjz-j-02-0-UI-s1 NCI CGAP Ftl Homo sapiens cDNA clone
UI-H-Ftl-bjz-j-02-0-UI 3', mRNA sequence.

CD370914
CD370914.1 GI:31155004
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 618)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ftl-bjz-j-02-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ftl"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site: 1: ECOR I; Site 2: Not I;
NCI CGAP Ftl is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCATCCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-Ftl
TAG_SEQ=GGCATCCGCG"

ORIGIN
Query Match      59.3%; Score 593.8; DB 14; Length 618;
Best Local Similarity 99.5%; Pred. No. 7.1e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 GCTGTACCCAGAGTCTCTGTGTAATGGGACTCAATCCCTAGGCGTGGCAGAAAGGG 60

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Db      611 GCTGTACCCAGAGTCTCTGTGTAATGGGACTCAATCCCTAGGCGTGGCAGAAAGGG 552
QY      61 AACAGAAAGGTTTTTTCAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACACCAATGCC 120
Db      551 AACAGAAAGGTTTTTTCAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACACCAATGCC 492
QY      121 CAACTGCTGCTTATAGGTTAGTGTCTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCTCAG 180
Db      491 CAACTGCTGCTTATAGGTTAGTGTCTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCTCAG 432
QY      181 CTCTCTCTCTTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTGAGCCAGGCGCTCTCTCAGCTCTC 240
Db      431 CTCTCTCTCTTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTGAGCCAGGCGCTCTCTCAGCTCTC 372
QY      241 CTACTCACTTAAAGCCCGCTGACAGAAACACGCGCCACATTTGGTTCTAAGAAAACCCCTC 300
Db      371 CTACTCACTTAAAGCCCGCTGACAGAAACACGCGCCACATTTGGTTCTAAGAAAACCCCTC 312
QY      301 TGTCTATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTATTATT 360
Db      311 TGTCTATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTATTATT 252
QY      361 GTTTGTTTTGATTCATTTGCTCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 420
Db      251 GTTTGTTTT-ATTCATTTGCTCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 193
QY      421 AAAGAGCCCTAGTTTTTATAGCTATGGAAATCAATTTCAATTTGGAGCTGGTGTCTCTCTTT 480
Db      192 AAAGAGCCCTAGTTTTTATAGCTATGGAAATCAATTTCAATTTGGAGCTGGTGTCTCTCTTT 133
QY      481 AAATCAAGTCCCTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAATTAATGGGATA 540
Db      132 AAATCAAGTCCCTTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTAATTAATGGGATA 73
QY      541 TTTATAAATGAGCAAAATATGATPACTGTTCATGTTCGAAATTAACCTCTCTCTCTCTCTCT 600
Db      72 TTTATAAATGAGCAAAATATCATCTGTTCAATGTTCGAAATTAACCTCTCTCTCTCTCTCT 13
QY      601 AAAAAAAAA 609
Db      12 AAAAAAAAA 4

RESULT 5
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CA431510      668 bp      mRNA      linear      EST 07-NOV-2002
UI-H-Ftl-bhm-i-17-0-UI-s1 NCI CGAP FTO Homo sapiens cDNA clone
UI-H-Ftl-bhm-i-17-0-UI 3', mRNA sequence.

CA431510
CA431510.1 GI:24794230
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 668)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.

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FEATURES	Location/Qualifiers	
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source	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="UI-H-F71-bhm-i-17-0-UI"	
	/tissue_type="Alveolar Macrophage"	
	/dev_stage="Adult"	
	/lab_host="DH10B (Life Technologies)"	
	/clone_lib="NCI CGAP F70"	
	/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP F70 is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa."	
	TAG_TISSUE=Human Lung Alveolar Macrophage	
	TAG_LIB=UI-H-F70	
	TAG_SEQ=GGCCATGCCG"	
ORIGIN	59.3%; Score 593.8; DB 14; Length 668;	
	Best local Similarity 99.5%; Pred. No. 6.8e-108;	
	Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;	
Qy	1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCGAAGGG 60	
	Db 611 GCTGTACCCAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCGAAGGG 552	
	Qy 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCTGAGCTTCTCTGTGTCTACACCAATGCC 120	
Db	551 AACAGAAAGGTTTTTGTAGTACGGCTATAGCTGAGCTTCTCTGTGTCTACACCAATGCC 492	
	Qy 121 CAATGCTGCTGTAGGCTGTAGTGTAAAGAGATCTCTGTCCTCAATCAGCCAGGACAGTCAG 180	
	Db 491 CAATGCTGCTGTAGGCTGTAGTGTAAAGAGATCTCTGTCCTCAATCAGCCAGGACAGTCAG 432	
Qy	181 CTCTCTCTTTTACGGCCAAATCCCGACCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 240	
	Db 431 CTCTCTCTTTTACGGCCAAATCCCGACCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 372	
	Qy 241 CTACTCACTTAAGCCCGCTGACAGAAACACGCCACATTTGGTTCTAAGAAACCCCTC 300	
Db	371 CTACTCACTTAAGCCCGCTGACAGAAACACGCCACATTTGGTTCTAAGAAACCCCTC 312	
	Qy 301 TGTCAATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360	
	Db 311 TGTCAATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 252	
Qy	361 GTTTGTTTGTGATTCATTTGCTATTTTATTAAGGGGGGCAAGAGTAGCAGTGTCTGTA 420	
	Db 251 GTTTGTTTGTGATTCATTTGCTATTTTATTAAGGGGGGCAAGAGTAGCAGTGTCTGTA 193	
	Qy 421 AAAGAGCTAGTTTTTATAGTACTGGAATCAATTTCAATTTGACTGGTGTGCTCTCTTT 480	
Db	192 AAAGAGCTAGTTTTTATAGTACTGGAATCAATTTCAATTTGACTGGTGTGCTCTCTTT 133	
	Qy 481 AAATCAAGTCTTTTAATTAACACTGAAATATATATAGCTAGATTTTAAATGGGAATA 540	
	Db 132 AAATCAAGTCTTTTAATTAAGACTGAAATATATATAGCTAGATTTTAAATGGGAATA 73	
Qy	541 TTTTAAATGAGCAAAATGATCTGTTCAATGTTCTGGAATAAACTTCACTGAAGAA 600	
	Db 1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCGAAGGG 60	
	Qy 1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCGAAGGG 60	
Db	601 AAAAAA 609	
	Db 12 AAAAAA 4	
Qy	72 TTTATAAATGAGCAAAATATCATCTGTTCAATGCTTCTGAATAAATCACTCTCAAGAA 13	
	Db 601 AAAAAA 609	
	Db 12 AAAAAA 4	
RESULT 6	CA307004 671 bp mRNA linear EST 01-NOV-2002	
	LOCUS UI-H-F71-bhu-c-24-0-UI.s1 NCI CGAP F71 Homo sapiens cDNA clone	
	DEFINITION UI-H-F71-bhu-c-24-0-UI 3', mRNA sequence.	
ACCESSION	CA307004	
	VERSION CA307004.1 GI:24470058	
	KEYWORDS EST.	
SOURCE	Homo sapiens (human)	
	ORGANISM Homo sapiens	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 671)	
	AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
	COMMENT Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-remail.nih.gov	
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I	
	cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa	
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
	Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu	
	The following repetitive elements were found in this cDNA	
	sequence: 221-272, >(TAAA)n#Simple_repeat	
	Seq primer: M13 FORWARD	
	POLYA=Yes.	
FEATURES	Location/Qualifiers	
	1..671	
	/organism="Homo sapiens"	
source	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="UI-H-F71-bhu-c-24-0-UI"	
	/tissue_type="Alveolar Macrophage"	
	/dev_stage="Adult"	
	/lab_host="DH10B (Life Technologies)"	
	/clone_lib="NCI CGAP F71"	
	/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP F71 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was	
	normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa."	
	TAG_TISSUE=Human Lung Alveolar Macrophage	
	TAG_LIB=UI-H-F71	
	TAG_SEQ=GGCCATGCCG"	
ORIGIN	59.3%; Score 593.8; DB 14; Length 671;	
	Best local Similarity 99.5%; Pred. No. 6.8e-108;	
	Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;	
Qy	1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCGAAGGG 60	
	Db 1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCGAAGGG 60	
	Qy 1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCGAAGGG 60	

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Db 611 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCAGAAAGGG 552
QY 61 AACAGAAAGGTTTTTGAAGTACGGCTATAGCCTGGACTTTCCTGTGTCTACACCAATGCC 120
Db 551 AACAGAAAGGTTTTTGAAGTACGGCTATAGCCTGGACTTTCCTGTGTCTACACCAATGCC 492
QY 121 CAACTGCCTGCTTAGGCTAGTGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCAG 180
Db 491 CAACTGCCTGCTTAGGCTAGTGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCAG 432
QY 181 CTCCTCTCTCTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 240
Db 431 CTCCTCTCTCTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 372
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCCACATTTGGTTCTAAGAAACCCCTC 312
QY 301 TGTCAATTCGCTCCACATCTGTAGTACGACCAACCGCTTCCCTATTTATTATTATTGTTT 360
Db 311 TGTCAATTCGCTCCACATCTGTAGTACGACCAACCGCTTCCCTATTTATTATTATTGTTT 252
QY 361 GTTTGTTTGTATTCATTTGGTCTAAATTTATTTCAAAGGGGGCAAGAGTAGCAGTCTGTGA 420
Db 251 GTTTGTTT - ATTCAATTCGTTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTCTGTGA 193
QY 421 AAAGAGCCTAGTTTTTAAATAGCTATGAGTCAATCAATTTGGACTGGTGTCTCTTTT 480
Db 193 AAAGAGCCTAGTTTTTAAATAGCTATGAGTCAATCAATTTGGACTGGTGTCTCTTTT 133
QY 481 AAATCAAGTCTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 73
Db 73 TTTTAAATGAGCAAAATATACATCTGTTCAATGGTTCTGAAATAACTTCACTGAAGAAA 13
QY 601 AAAAAAAAAA 609
Db 12 AAAAAAAAAA 4

RESULT 7
LOCUS BU626429/c
DEFINITION UI-H-FT0-bhm-g-02-0-UI-s1 NCI CGAP_FTO Homo sapiens cDNA clone
ACCESSION BU626429
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
NCI-CCAG http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robert-Pamela, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
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/clone="UI-H-FT0-bhm-g-02-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FTO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_FTO is a cDNA library constructed from a pool of
81 RNA samples from Alveolar Macrophages challenged with
different treatments. The library was constructed
according to Bonaïdo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GGCATGCGG. The cell line
was provided by Gary W. Hunninghake from the University of
Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT0
TAG_SEQ=GGCATGCGG"

ORIGIN
Query Match 59.3%; Score 593.8; DB 13; Length 701;
Best Local Similarity 99.5%; Pred. No. 6.7e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCAGAAAGGG 60
Db 611 GGTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCAGAAAGGG 552
QY 61 AACAGAAAGGTTTTTGAAGTACGGCTATAGCCTGGACTTTCCTGTGTCTACACCAATGCC 120
Db 551 AACAGAAAGGTTTTTGAAGTACGGCTATAGCCTGGACTTTCCTGTGTCTACACCAATGCC 492
QY 121 CAACTGCCTGCTTAGGCTAGTGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCAG 180
Db 491 CAACTGCCTGCTTAGGCTAGTGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCAG 432
QY 181 CTCCTCTCTCTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 240
Db 431 CTCCTCTCTCTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACTCTC 372
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCCACATTTGGTTCTAAGAAACCCCTC 312
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Db 311 TGTCAATTCGCTCCACATCTGTAGTACGACCAACCGCTTCCCTATTTATTATTATTGTTT 252
QY 361 GTTTGTTTGTATTCATTTGGTCTAAATTTATTTCAAAGGGGGCAAGAGTAGCAGTCTGTGA 420
Db 251 GTTTGTTT - ATTCAATTCGTTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTCTGTGA 193
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QY 481 AAATCAAGTCTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
Db 132 AAATCAAGTCTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 73
QY 541 TTTTAAATGAGCAAAATATACATCTGTTCAATGGTTCTGAAATAACTTCACTGAAGAAA 600
Db 72 TTTTAAATGAGCAAAATATACATCTGTTCAATGGTTCTGAAATAACTTCACTGAAGAAA 13
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QY 601 AAAAAAAAAA 609
Db 12 AAAAAAAAAA 4

RESULT 8
BU626613/c 704 bp mRNA linear EST 23-SEP-2002
LOCUS UI-H-FT0-bhm-j-10-0-UI.s1 NCI CGAP FTO Homo sapiens cDNA clone
DEFINITION UI-H-FT0-bhm-j-10-0-UI 3', mRNA sequence.
ACCESSION BU626613.1 GI:23292828
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bentso-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..704
location=Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT0-bhm-j-10-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTO"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTO is a cDNA library constructed from a pool of
81 RNA samples from Alveolar Macrophages challenged with
different treatments. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GGCATGCCG. The cell line
was provided by Gary W. Hunninghake from the University of
Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 59.3%; Score 593.8; DB 13; Length 704;
Best Local Similarity 99.5%; Pred. No. 6.6e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 60
Db 611 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 552

61 AACAGAAAGTTTGTAGTAGCGCTATAGCTTGACCTTCTCTGTCTACCAATGCC 120
551 AACAGAAAGTTTGTAGTAGCGCTATAGCTTGACCTTCTCTGTCTACCAATGCC 492
121 CAATCGCTGCTTAGGTAGTGTAGAGGATCTCTGTCTCCATCAGCAGGACAGTCAG 180
491 CAATCGCTGCTTAGGTAGTGTAGAGGATCTCTGTCTCCATCAGCAGGACAGTCAG 432
181 CTCTCTCTCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGTAGCAGGCTCTCTCACTCTC 240
431 CTCTCTCTCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGTAGCAGGCTCTCTCACTCTC 372
241 CTACTCACTTAAAGCCCGCTGACAGAAACCAAGCCGACATTTGGTCTTAGAAACCTC 300
371 CTACTCACTTAAAGCCCGCTGACAGAAACCAAGCCGACATTTGGTCTTAGAAACCTC 312
301 TGTCAATTCGCTCCACATTCGTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTT 360
311 TGTCAATTCGCTCCACATTCGTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTT 252
361 GTTGTGTTGATTCATTCGCTCTAAATTTTCAAGGGGGGCAAGTAGCAGTCTCTGTA 420
251 GTTGTGTTT-ATTCAATTCGCTCTAAATTTTCAAGGGGGGCAAGTAGCAGTCTCTGTA 193
421 AAAGAGCCTAGTCTTTTAATAGCTATGGAATCAATTTCAATTTGGAGTGTGCTCTCTTT 480
192 AAAGAGCCTAGTCTTTTAATAGCTATGGAATCAATTTCAATTTGGAGTGTGCTCTCTTT 133
481 AAATCAAGTCTTTTAATTAACACATGAAATATATAAGCTCAGATTATTAAATGGGAATA 540
132 AAATCAAGTCTTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 73
541 TTATTAATAGCAATATGATCTGTTCAATGTTCTGAAATAACTTCACTGAAGAAA 600
72 TTATTAATAGCAATATGATCTGTTCAATGTTCTGAAATAACTTCACTGAAGAAA 13

601 AAAAAAAAAA 609
12 AAAAAAAAAA 4

RESULT 9
BU626909/c 706 bp mRNA linear EST 23-SEP-2002
LOCUS UI-H-FT0-bhm-h-03-0-UI.s1 NCI CGAP FTO Homo sapiens cDNA clone
DEFINITION UI-H-FT0-bhm-h-03-0-UI 3', mRNA sequence.
ACCESSION BU626909
VERSION BU626909.1 GI:23293124
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 706)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bentso-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..706
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-bhn-h-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="NCI CGAP FTO"
/modified="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTO is a cDNA library constructed from a pool of
81 RNA samples from Alveolar Macrophages challenged with
different treatments. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GGCATGCCG. The cell line
was provided by Gary W. Hunninghake from the University of
Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match          59.3%; Score 593.8; DB 13; Length 706;
Best Local Similarity 99.5%; Pred. No. 6.6e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCAGAGAGTCTGTGCTGAATGTGGATCAATCCCTAGGCTGCAGAAAGG 60
DB 611 GCTGTACCAGAGAGTCTGTGCTGAATGTGGATCAATCCCTAGGCTGCAGAAAGG 552
QY 61 AACAGAAAGGTTTTGAGTACGGCTATAGCTGTGACCTTCTGCTGTGCTACACCAATGCC 120
DB 551 AACAGAAAGGTTTTGAGTACGGCTATAGCTGTGACCTTCTGCTGTGCTACACCAATGCC 492
QY 121 CAATGCTGCTTAGGTAGTGTAAAGAGGATCTCTGTCCATACCCAGGACAGTCAG 180
DB 491 CAATGCTGCTTAGGTAGTGTAAAGAGGATCTCTGTCCATACCCAGGACAGTCAG 432
QY 181 CTCTCTCTTTTTCAGGGCCAAATCCCGACCTTTTGTGAGCCAGGCTCTCTACCTCTC 240
DB 431 CTCTCTCTTTTTCAGGGCCAAATCCCGACCTTTTGTGAGCCAGGCTCTCTACCTCTC 372
QY 241 CTACTCACTTAAAGCCGCTGACAGAAACCCAGCCACACATTTGGTTCTAAGAAACCCCTC 300
DB 371 CTACTCACTTAAAGCCGCTGACAGAAACCCAGCCACACATTTGGTTCTAAGAAACCCCTC 312
QY 301 TGTCAATGCTCCACATTCGTAGTACGACCGCTTCCCTATTATTATTATTATTGTTT 360
DB 311 TGTCAATGCTCCACATTCGTAGTACGACCGCTTCCCTATTATTATTATTATTGTTT 252
QY 361 GTTTGTTTGTATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA 420
DB 251 GTTTGTTTGTATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA 193
QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTGACCTGGTGTGCTCTCTTT 480
DB 192 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTGACCTGGTGTGCTCTCTTT 133
QY 481 AAATCAAGTCTCTTTAATTAACACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATA 540
DB 132 AAATCAAGTCTCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATA 73
QY 541 TTTTATAATAGCAAAATAGATAGTCTCAATAGGTTCTGAAATTAACCTTCACTTGAAGAAA 600
DB 72 TTTTATAATAGCAAAATATCATACTGTTTCAATAGGTTCTGAAATTAACCTTCACTTGAAGAAA 13

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QY 601 AAAAAAAAAA 609
DB 12 AAAAAAAAAA 4

RESULT 10
CA305984/c
LOCUS
DEFINITION
  UI-H-FTI-bhs-f-05-0-UI.s1 NCI CGAP FTO Homo sapiens cDNA clone
  UI-H-FTI-bhs-f-05-0-UI 3', mRNA sequence.
ACCESSION
  CA305984
VERSION
  CA305984.1 GI:24469035
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 767)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Unpublished (1997)
  Tumor Gene Index
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs@mail.nih.gov
  Tissue Procurement: Dr. Gary W. Hunninghake, U of I
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bent-soares@uiowa.edu
  The following repetitive elements were found in this cDNA
  sequence: 221-272: s(TAAA)n#Simple_repeat
  Seq primer: M13 FORWARD
  POLYA=yes.

FEATURES
    Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="UI-H-FTI-bhs-f-05-0-UI"
        /tissue_type="Alveolar Macrophage"
        /dev_stage="Adult"
        /lab_host="NCI CGAP FTO"
        /clone_lib="NCI CGAP FTO"
        /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
        modified polylinker; Site 1: EcoR I; Site 2: Not I;
        NCI CGAP FTO is a normalized cDNA library constructed from
        a pool of 81 RNA samples from Alveolar Macrophages
        challenged with different treatments. The library was
        normalized according to Bonaldo, Lennon and Soares, Genome
        Research, 6:791-806, 1996. First strand cDNA synthesis was
        primed with an oligo-dT primer containing a Not I site.
        Double stranded cDNA was ligated to an EcoR I adaptor,
        digested with Not I, and cloned directionally into
        pT7T3-Pac vector. The oligonucleotide used to prime the
        synthesis of first-strand cDNA contains a library tag
        sequence that is located between the Not I site and the
        (dT)18 tail. The sequence tag for this library is
        GGCATGCCG. The tissue was provided by Dr. Gary W.
        Hunninghake of the University of Iowa.
        TAG_TISSUE=Human Lung Alveolar Macrophage
        TAG_LIB=UI-H-FTI
        TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match          59.3%; Score 593.8; DB 14; Length 767;
Best Local Similarity 99.5%; Pred. No. 6.4e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCAGAGAGTCTGTGCTGAATGTGGATCAATCCCTAGGCTGCAGAAAGG 60
DB 611 GCTGTACCAGAGAGTCTGTGCTGAATGTGGATCAATCCCTAGGCTGCAGAAAGG 552

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QY	61	AAAGAAAGGTTTTTGGTACGGCTATAGCTGGACTTTCCTGTGTCTACACCAATGCC	120
Db	551	AAAGAAAGGTTTTTGGTACGGCTATAGCTGGACTTTCCTGTGTCTACACCAATGCC	492
QY	121	CAACTGCTGCTTAGGTAGTCTAAGAGGATCTCTGTCATCAGCCAGGACAGTCTAG	180
Db	491	CAACTGCTGCTTAGGTAGTCTAAGAGGATCTCTGTCATCAGCCAGGACAGTCTAG	432
QY	181	CTCTCTCTTTTCAAGGCGCAATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	240
Db	431	CTCTCTCTTTTCAAGGCGCAATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	372
QY	241	CTACTCACTTAAAGCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC	300
Db	371	CTACTCACTTAAAGCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC	312
QY	301	TGTCATTCGCTCCACATTTCTGATGAGCAACCCGCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	360
Db	311	TGTCATTCGCTCCACATTTCTGATGAGCAACCCGCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	352
QY	361	GTITGTTTTGATTCATTTGCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTA	420
Db	251	GTITGTTTT-ATTCATTTGCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTA	193
QY	421	AAAGAGCTAGTTTTTAAATGAGCAACCCGCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	480
Db	192	AAAGAGCTAGTTTTTAAATGAGCAACCCGCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	133
QY	481	AAATCAAGTCTTTTAAATGAGCAACCCGCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	540
Db	132	AAATCAAGTCTTTTAAATGAGCAACCCGCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	73
QY	541	TTTATAAATGAGCAACCAATATGATGAGTCTCTCAATGGTTCTGAATTAATCACTTCACTGAGAA	600
Db	72	TTTATAAATGAGCAACCAATATGATGAGTCTCTCAATGGTTCTGAATTAATCACTTCACTGAGAA	13
QY	601	AAAAAATA 609	
Db	12	AAAAAATA 4	
RESULT 11			
CA442834/c			
LOCUS			
DEFINITION			
UI-H-DP0-avr-h-12-0-UI s1 NCI CGAP Fsl Homo sapiens CDNA clone			
UI-H-DP0-avr-h-12-0-UI 3', mRNA sequence.			
CA442834			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 767)			
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
Tumor Gene Index			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapsb@mail.nih.gov			
Tissue Procurement: Dr. Mary Hendrix			
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa			
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa			
Clone Distribution: Clone distribution information can be obtained			
from Dr. M. Bento Soares, bento-soares@uiowa.edu			
The following repetitive elements were found in this cDNA			
sequence: 221-272, >(TAA)n#Simple_repeat			
Seq primer: M13 FORWARD			
POLVA=Yes.			
FEATURES			
Location/Qualifiers			
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/organism="Homo sapiens"			

/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="UI-H-DP0-avr-h-12-0-UI"			
/tissue_type="fibrosarcoma"			
/lab_host="DH10B (Life Technologies)"			
/clone_lib="NCI CGAP Fsl"			
/note="Vector: p773-pac (Pharmacia) with a modified			
polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Fsl is			
a cDNA library containing the following tissue(s):			
Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The			
library was constructed according to Bonaldo, Lennon and			
Soares, Genome Research, 6:791-806, 1996. First strand			
cDNA synthesis was primed with an oligo-dT primer			
containing a Not I site. Double stranded cDNA was ligated			
to an EcoR I adaptor, digested with Not I, and cloned			
directionally into p773-pac vector. The oligonucleotide			
used to prime the synthesis of first-strand cDNA contains			
a library tag sequence that is located between the Not I			
site and the (dT)18 tail. The sequence tag for this			
library is GTTCTACGAG.			
TAG TISSUE=fibrosarcoma			
TAG_LIB=UI-H-DP0			
TAG_SEQ=GTTCACGAG"			

ORIGIN

Query Match		59.3%;	Score 593.8;	DB 14;	Length 767;
Best Local Similarity		99.5%;	Pred. No. 6.4e-108;		
Matches 606;		Conservative	0;	Mismatches	2;
				Indels	1;
				Gaps	1;
QY	1	GCTGTACCCAGAGAGTCTGTGCTGAATGTGAGCTCAATCCTAGGGCTGGCAGAAAGG	60		
DB	611	GCTGTACCCAGAGAGTCTGTGCTGAATGTGAGCTCAATCCTAGGGCTGGCAGAAAGG	552		
QY	61	AAAGAGAGGTTTTTGTAGTACGGCTATAGCTGGAGCTTTCCTGTGTCTACACCAATGCC	120		
DB	551	AAAGAGAGGTTTTTGTAGTACGGCTATAGCTGGAGCTTTCCTGTGTCTACACCAATGCC	492		
QY	121	CAACTGCTGCTTAGGGTAGTCTAAGAGGATCTCTGTTCATCAGCAGGACAGTCTAG	180		
DB	491	CAACTGCTGCTTAGGGTAGTCTAAGAGGATCTCTGTTCATCAGCAGGACAGTCTAG	432		
QY	181	CTCTCTCTTTTTCAGGGCCAAATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	240		
DB	431	CTCTCTCTTTTTCAGGGCCAAATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	372		
QY	241	CTACTCACTTAAAGCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC	300		
DB	371	CTACTCACTTAAAGCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC	312		
QY	301	TGTCATTCGCTCCACATTTCTGATGAGCAACCCGCTTCCCTATTATTATTATTATTGTTT	360		
DB	311	TGTCATTCGCTCCACATTTCTGATGAGCAACCCGCTTCCCTATTATTATTATTATTGTTT	252		
QY	361	GTITGTTTTGATTCATTTGCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTA	420		
DB	251	GTITGTTTTT-ATTCATTTGCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTA	193		
QY	421	AAAGAGCTAGTTTTTAAATGAGCAACCAATTCATTTGGAGCTGGTGTCTCTCTTT	480		
DB	192	AAAGAGCTAGTTTTTAAATGAGCAACCAATTCATTTGGAGCTGGTGTCTCTCTTT	133		
QY	481	AAATCAAGTCTTTTAAATGAGCAACCAATATATAAGCTCAGATTATTAAATGGGAATA	540		
DB	132	AAATCAAGTCTTTTAAATGAGCAACCAATATATAAGCTCAGATTATTAAATGGGAATA	73		
QY	541	TTTATAAATGAGCAAAATATGATGAGTCTCAATGGTTCTGAAATAAACTTCACTGAGAAA	600		
DB	72	TTTATAAATGAGCAAAATATGATGAGTCTCAATGGTTCTGAAATAAACTTCACTGAGAAA	13		
QY	601	AAAAAAAAA 609			
DB	12	AAAAAAAAA 4			

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RESULT 12
BQ000281/c
LOCUS
DEFINITION
  BQ000281 770 bp mRNA linear EST 17-JUN-2002
  IMAGE:5883972 3', mRNA sequence.
ACCESSION
  BQ000281
VERSION
  BQ000281.1 GI:19725181
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  1 (bases 1 to 770)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. Mary Hendrix
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be found
  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
  The following repetitive elements were found in this cDNA
  sequence: 221-272, >(TAAA)n#Simple_repeat
  Seq primer: M13 FORWARD
  POLYA=Yes.
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  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="IMAGE:5883972"
  /tissue_type="Fibroblast"
  /lab_host="DH10B (Life Technologies)"
  /clone_lib="NCI CGAP Fsl"
  /note="Vector: p773-Pac (Pharmacia) with a modified
  polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Fsl is
  a cDNA library containing the following tissue(s):
  Fibrosarcoma Cell line HT-1080 (ATCC number CCL-121). The
  library was constructed according to Bonaldi, Lennon and
  Soares, Genome Research, 6:791-806, 1996. First strand
  cDNA synthesis was primed with an oligo-dT primer
  containing a Not I site. Double stranded cDNA was ligated
  to an EcoR I adaptor, digested with Not I, and cloned
  directionally into p773-Pac vector. The oligonucleotide
  used to prime the synthesis of first-strand cDNA contains
  a library tag sequence that is located between the Not I
  site and the (dT)18 tail. The sequence tag for this
  library is GTTCTACGAG.
  TAG TISSUE=fibroblast
  TAG_LIB=UI-H-DPO
  TAG_SEQ=GTCTACGAG"
ORIGIN
Query Match 59.3%; Score 593.8; DB 12; Length 770;
Best Local Similarity 99.5%; Pred. No. 6.4e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GCTGTACCCAGAGAGTCTCTGTCTGATGGACTCAATCCCTAGGGCTGGCAGAAAGG 60
Db 611 GCTGTACCCAGAGAGTCTCTGTCTGATGGACTCAATCCCTAGGGCTGGCAGAAAGG 552
QY 61 AACAGAAAGGTTTTAGTACGGCTATAGCTCGACTTTCTCTGTCTACCAATGCC 120
Db 551 AACAGAAAGGTTTTAGTACGGCTATAGCTCGACTTTCTCTGTCTACCAATGCC 492
QY 121 CAATCGCTCCCTTAGGGTAGTCTTAAGAGATCTCTGTCCATCAGCCAGGACAGTCTAG 180
Db 491 CAATCGCTCCCTTAGGGTAGTCTTAAGAGATCTCTGTCCATCAGCCAGGACAGTCTAG 432

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/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTO is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drl)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GGCCATGCCG"

ORIGIN		Query Match	59.3%;	Score 593.8;	DB 14;	Length 777;	
		Best Local Similarity	99.5%;	Pred. No. 6.3e-108;			
		Mismatches	606;	Conservative	0;	Mismatches	2; Indels 1; Gaps 1;
Qy	1	GCTGTACCCAGAGAGTCTCTGCTGATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	60				
Db	611	GCTGTACCCAGAGAGTCTCTGCTGATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	552				
Qy	61	AACAGAAAGTTTTTGAGTACGGCTATAGCTGGACTTTCTCTGTCTACACCAATGCC	120				
Db	551	AACAGAAAGTTTTTGAGTACGGCTATAGCTGGACTTTCTCTGTCTACACCAATGCC	492				
Qy	121	CAACTGCTCCCTAGGTTAGTCTAAGAGATCTCTGTCCATAGCCAGGACAGTCAG	180				
Db	491	CAACTGCTCCCTAGGTTAGTCTAAGAGATCTCTGTCCATAGCCAGGACAGTCAG	432				
Qy	181	CTCTCTCTTTCAGGCGCAATCCCGACCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC	240				
Db	431	CTCTCTCTTTCAGGCGCAATCCCGACCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC	372				
Qy	241	CTACTCACTTAAAGCCCGCTGACAGAAACACGGCCACATTTGGTCTTAAGAAACCTC	300				
Db	371	CTACTCACTTAAAGCCCGCTGACAGAAACACGGCCACATTTGGTCTTAAGAAACCTC	312				
Qy	301	TGTCATTGCTCCACATTCGTAGACCAACCGCTTCCCTATTATTATTATTATTGTTT	360				
Db	311	TGTCATTGCTCCACATTCGTAGACCAACCGCTTCCCTATTATTATTATTATTGTTT	252				
Qy	361	GTGTTGTTTTCATTTGTTGTTTAAATTTTATCAAGGGGGCAAGAGTAGAGTGTCTGTA	420				
Db	251	GTGTTGTTT-ATTCAATTTGTTTAAATTTTATCAAGGGGGCAAGAGTAGAGTGTCTGTA	193				
Qy	421	AAAGAGCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTT	480				
Db	192	AAAGAGCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTT	133				
Qy	481	AAATCAAGTCTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	540				
Db	132	AAATCAAGTCTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	73				
Qy	541	TTTATAATAGCAAAATATGATCTGTTCAATGTTCTGAAATAAATCACTCAGAGAAA	600				
Db	72	TTTATAATAGCAAAATATGATCTGTTCAATGTTCTGAAATAAATCACTCAGAGAAA	13				
Qy	601	AAAAAANA 609					
Db	12	AAAAAANA 4					
RESULT 14		CA307234/c	798 bp	mRNA	linear	EST	01-NOV-2002
LOCUS		CA307234					

DEFINITION UI-H-FTI-bhu-p-02-0-UI.s1 NCI CGAP_FTI Homo sapiens cDNA clone
UI-H-FTI-bhu-p-02-0-UI 3', mRNA sequence.
ACCESSION CA307234
VERSION CA307234.1 GI:24470288
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 798)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bent-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-bhu-p-02-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP_FTI"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drl)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	59.3%;	Score 593.8;	DB 14;	Length 798;
Best Local Similarity	99.5%;	Pred. No. 6.3e-108;		
Mismatches	606;	Conservative	0;	Mismatches 2; Indels 1; Gaps 1;
Qy	1	GCTGTACCCAGAGAGTCTCTGCTGATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	60	
Db	611	GCTGTACCCAGAGAGTCTCTGCTGATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	552	
Qy	61	AACAGAAAGTTTTTGAGTACGGCTATAGCTGGACTTTCTCTGTGTCTACACCAATGCC	120	
Db	551	AACAGAAAGTTTTTGAGTACGGCTATAGCTGGACTTTCTCTGTGTCTACACCAATGCC	492	
Qy	121	CAACTGCTCCCTAGGTTAGTCTAAGAGATCTCTGTCCATAGCCAGGACAGTCAG	180	
Db	491	CAACTGCTCCCTAGGTTAGTCTAAGAGATCTCTGTCCATAGCCAGGACAGTCAG	432	

QY 181 CTCCTCTCTTTTTCAGGGCCCAATCCCGAGCCCTTTTTCAGCCAGCCCTCTCTCACCTCTC 240
 Db 431 CTCCTCTCTTTTTCAGGGCCCAATCCCGAGCCCTTTTTCAGCCAGCCCTCTCTCACCTCTC 372
 QY 241 CTACTCACTTAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTTAAGAACCCCTC 300
 Db 371 CTACTCACTTAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTTAAGAACCCCTC 312
 QY 301 TGTCAATCGCTCCCACTTCATGATGAGCAACCGCTTCCTCTATTATTATTATTATTGTTT 360
 Db 311 TGTCAATCGCTCCCACTTCATGATGAGCAACCGCTTCCTCTATTATTATTATTATTGTTT 252
 QY 361 GTTTCGTTTGTATCTATTCGTTCTAATTTTTCAGGGGGGCAAGTAGCGAGTCTCTGTA 420
 Db 251 GTTTCGTTT-ATTCAATCGTTCTAATTTTTCAGGGGGGCAAGTAGCGAGTCTCTGTA 193
 QY 421 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 480
 Db 192 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 133
 QY 481 AAATCAAGTCTTTAAATTAACACTGAAATATATAAGCTCAGATATTAAATGGGAATA 540
 Db 132 AAATCAAGTCTTTAAATTAAGACTGAAATATATAAGCTCAGATATTAAATGGGAATA 73
 QY 541 TTTTAAATGAGCAATATGATATCTGTTCAATGGTTCCTGAATTAACCTTCACTGAAGAAA 600
 Db 72 TTTTAAATGAGCAATATGATATCTGTTCAATGGTTCCTGAATTAACCTTCACTGAAGAAA 13
 QY 601 AAAAAAAAAA 609
 Db 12 AAAAAAAAAA 4

RESULT 15
 BQ001221/c
 LOCUS
 DEFINITION
 IMAGE:5892524 3', mRNA sequence.
 ACCESSION
 VERSION
 BQ001221.1 GI:19726121
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 703)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Cloning Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 The following repetitive elements were found in this cDNA
 sequence: 221-272, >(TAAA)nSimple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source
 Location/Qualifiers
 1..703
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5892524"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP DH1"
 /notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP DH1 is a normalized cDNA library containing the
 following tissue(s): VS-8 Cell line from Metastatic
 Chondrosarcoma in Lung. The library was constructed
 according to Bernaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is AGATCATTGC.
 TAG_TISSUE=lung
 TAG_LIB=UI-H-DH1
 TAG_SEQ=AGATCATTGC"

ORIGIN

Query Match 59.2%; Score 592.8; DB 12; Length 703;
 Best Local Similarity 99.3%; Pred. No. 1.1e-107;
 Matches 605; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 GCTGTACCCAGAGAGTCCTGTCTCAATGTGAGCTCAATCCCTAGGGCTGCAGAAAGGG 60
 Db 611 GCTGTACCCAGAGAGTCCTGTCTCAATGTGAGCTCAATCCCTAGGGCTGCAGAAAGGG 552
 QY 61 AACAGAAAGGTTTTGAGTAGCGCTATAGCCTGGACTTTTCCTGTTGTCTACCAATGCC 120
 Db 551 AACAGAAAGGTTTTGAGTAGCGCTATAGCCTGGACTTTTCCTGTTGTCTACCAATGCC 492
 QY 121 CAACCTGCTGCTTAGGCTAGTCTTAAGAGATCTCTGTCTCATCAGCCAGAGCAGTCAG 180
 Db 491 CAACCTGCTGCTTAGGCTAGTCTTAAGAGATCTCTGTCTCATCAGCCAGAGCAGTCAG 432
 QY 181 CTCCTCTCTTTTCAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGCCCTCTCTCACCTCTC 240
 Db 431 CTCCTCTCTTTTCAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGCCCTCTCTCACCTCTC 372
 QY 241 CTACTCACTTAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTTAAGAACCCCTC 300
 Db 371 CTACTCACTTAAGCCCGCTGACAGAAACACCGCCACATTTGGTTCTTAAGAACCCCTC 312
 QY 301 TGTCAATCGCTCCCACTTCATGATGAGCAACCGCTTCCTCTATTATTATTATTATTGTTT 360
 Db 311 TGTCAATCGCTCCCACTTCATGATGAGCAACCGCTTCCTCTATTATTATTATTATTGTTT 252
 QY 361 GTTTCGTTTGTATCTATTCGTTCTAATTTTTCAGGGGGGCAAGTAGCGAGTCTCTGTA 420
 Db 251 GTTTCGTTT-ATTCAATCGTTCTAATTTTTCAGGGGGGCAAGTAGCGAGTCTCTGTA 193
 QY 421 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 480
 Db 192 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 133
 QY 481 AAATCAAGTCTTTAAATTAACACTGAAATATATAAGCTCAGATATTAAATGGGAATA 540
 Db 132 AAATCAAGTCTTTAAATTAAGACTGAAATATATAAGCTCAGATATTAAATGGGAATA 73
 QY 541 TTTTAAATGAGCAATATGATATCTGTTCAATGGTTCCTGAATTAACCTTCACTGAAGAAA 600
 Db 72 TTTTAAATGAGCAATATGATATCTGTTCAATGGTTCCTGAATTAACCTTCACTGAAGAAA 13
 QY 601 AAAAAAAAAA 609
 Db 12 AAAAAAAAAA 4

Search completed: July 2, 2004, 13:27:46
 Job time : 2598 sec

GenCore version 5.1.4_p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 20:32:30 ; Search time 1145 Seconds
(without alignments)
5998.482 Million cell updates/sec
Title: US-09-247-874c-2_COPY_8710_8945
Perfect score: 236
Sequence: 1 ttgtgattcattgtctaat.....ataaacttcactgaagaaa 236

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_htg.*
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8: gb_pl.*
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10: gb_ro.*
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12: gb_sy.*
13: gb_un.*
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18: em_in.*
19: em_mu.*
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22: em_pat.*
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26: em_sts.*
27: em_un.*
28: em_vi.*
29: em_htg_hum.*
30: em_htg_inv.*
31: em_htg_other.*
32: em_htg_mus.*
33: em_htg_pln.*
34: em_htg_rod.*
35: em_htg_man.*
36: em_htg_vit.*
37: em_sy.*
38: em_htgo_hum.*
39: em_htgo_mus.*
40: em_htgo_other.*
41: em_htgo_mus.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	194	82.2	614	11	G10509	G10509 human STS C
2	194	82.2	656	6	AX027920	AX027920 Sequence
3	194	82.2	1469	6	I01156	I01156 Sequence 1
4	194	82.2	1496	9	HUMILI	K02770 Human monoc
5	194	82.2	1496	9	HUMILIC	M54933 Human monoc
6	194	82.2	1507	6	E00846	E00846 CDNA sequence
7	194	82.2	1507	6	I07942	I07942 Sequence 1
8	194	82.2	9721	6	AX052806	AX052806 Sequence
9	194	82.2	9721	6	AX067266	AX067266 Sequence
10	194	82.2	9721	6	AX469435	AX469435 Sequence
11	194	82.2	9721	9	HSILIB	X04500 Human gene
12	189	80.1	1382	6	AX119978	AX119978 Sequence
13	189	80.1	1473	9	HSPROIB	X56087 Human mRNA
14	189	80.1	1497	6	AR030386	AR030386 Sequence
15	189	80.1	1497	6	E06734	E06734 DNA encodn
16	189	80.1	1497	9	HUMILIBA	M15330 Human inter
17	189	80.1	1522	9	BC008678	BC008678 Homo sapi
18	189	80.1	17824	9	HUMILIB	M15840 Human inter
19	189	80.1	17447	9	AY137079	AY137079 Homo sapi
20	189	80.1	154214	9	AC079753	AC079753 Homo sapi
21	132	55.9	1514	6	AR086959	AR086959 Sequence 2
22	132	55.9	1514	6	I00729	I00729 Sequence 2
23	121	51.3	1404	6	A21148	A21148 PGIF- alpha
24	121	51.3	1404	6	E01230	E01230 CDNA encodi
25	121	51.3	1404	6	E11934	E11934 CDNA encodi
26	121	51.3	1404	6	E12090	E12090 Human cDNA
27	121	51.3	1404	6	I00228	I00228 Sequence 2
28	41	17.4	1458	6	E02498	E02498 CDNA encodi
29	30	12.7	400	11	G13631	G13631 SHGC-11912
30	22	9.3	1377	4	RAB11B	M26295 Rabbit inte
31	22	9.3	1403	4	RAB11B2	D21835 Rabbit mRNA
32	22	9.3	23104	2	AC017874	AC017874 Drosophil
33	22	9.3	171226	3	AC008144	AC008144 Drosophil
34	22	9.3	238245	3	AE003737	AE003737 Drosophil
35	21	8.9	150956	2	AC117259	AC117259 Mus muscu
36	21	8.9	155020	2	AC106390	AC106390 Rattus no
37	20	8.5	56870	9	AL512822	AL512822 Human DNA
38	20	8.5	59728	2	AC104252	AC104252 Rattus no
39	20	8.5	70849	2	AC090139	AC090139 Homo sapi
40	20	8.5	91242	9	AP001252	AP001252 Homo sapi
41	20	8.5	105495	9	AC105999	AC105999 Homo sapi
42	20	8.5	105496	9	AF165142	AF165142 Homo sapi
43	20	8.5	120038	9	AC020551	AC020551 Homo sapi
44	20	8.5	126117	2	AL57949	AL57949 Homo sapi
45	20	8.5	140409	2	AC044825	AC044825 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS human STS CHLC.UTR_00699_X04500.P37183 clone UTR_00699_X04500, 614 bp DNA linear STS 15-AUG-1995
DEFINITION sequence tagged site.
ACCESSION G10509
VERSION G10509.1 GI:942358
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker
Selected genomic DNA prepared from XY individual of French nationality.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 614)

AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: UTR_00699_X04500, CHLC.UTR_00699_X04500.T36097
 Contact: Dr. Jeffrey C. Murray
 UofI
 The University of Iowa
 Department of Pediatrics, Iowa City, IA 52242, USA
 Tel: (319) 356-3508
 Fax: (319) 356-3347
 Email: jeff-murray@uiowa.edu

Primer A: AGTCAGCTCTCTCTTCAGG
 Primer B: CTTGCCCTCTTTGAATAAT
 STS size: 229
 PCR Profile:

denature: 30 seconds at 94 degrees C
 annealing: 75 seconds at 55 degrees C
 extension: 15 seconds at 72 degrees C
 PCR cycles: 27
 extension: 6 minutes at 72 degrees C

Protocol:

Template: 30ng genomic DNA
 Primer: each 1.5 pmole
 dNTPs: each 200 uM
 Taq Polymerase: 0.3 units
 Total Vol: 10 uL

Buffer:

MgCl2: 1.5mM
 KCl: 50mM
 Tris: 10mM
 PH: 8.3

Prepared with primer pairs derived from X04500.

FEATURES
 source
 1..614
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 STS
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 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.9e-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 60
 Db 371 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 430
 QY 61 GCCTAGTTTTTAAGTCTATGCAATCAATTCATTTGGACTGGTGTCTCTTTAAATC 120
 Db 431 GCCTAGTTTTTAAGTCTATGCAATCAATTCATTTGGACTGGTGTCTCTTTAAATC 490
 QY 121 AAGTCCTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 180
 Db 491 AAGTCCTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 550
 QY 181 AAATGACCAATAT 194
 Db 551 AAATGACCAATAT 564
 RESULT 2
 AX027920
 LOCUS AX027920 656 bp DNA linear PAT 16-SEP-2000
 DEFINITION Sequence 5 from Patent WO0039314.
 ACCESSION AX027920
 VERSION AX027920.1 GI:10188746
 KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 656)
AUTHORS Kastelic, T. and Cheneval, D.
TITLE Assay for identifying compounds which affect stability of mrna
JOURNAL Patent: WO 0039314-A 5 06-JUL-2000;
 KASTELIC TANIA (CA); CHENEVAL DOMINIQUE (CA); NOVATION
 PHARMACEUTICALS INC (CA)
FEATURES
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 1..656
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 176 a 151 c 129 g 200 t
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 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 60
 Db 429 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 488
 QY 61 GCCTAGTTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 120
 Db 489 GCCTAGTTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 548
 QY 121 AAGTCCTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 180
 Db 549 AAGTCCTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 608
 QY 181 AAATGACCAATAT 194
 Db 609 AAATGACCAATAT 522
 RESULT 3
 LOCUS I01156 1469 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 1 from Patent US 4762914.
 ACCESSION I01156
 VERSION I01156.1 GI:313921
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
REFERENCE
 1 (bases 1 to 1469)
AUTHORS Auron, P.E., Webb, A.C., Gehrke, L., Dinarello, C.A., Rosenwasser, L.J.,
 Rich, A. and Wolff, S.M.
TITLE Truncated protein of interleukin-1
JOURNAL Patent: US 4762914-A 1 09-AUG-1988;
 119 Wilson Dr.; Framingham, MA
COMMENT On Jul 30, 1993 this sequence version replaced gi:285486.
FEATURES
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 Location/Qualifiers
 /organism="unknown"
 BASE COUNT 408 a 354 c 326 g 381 t
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 Best Local Similarity 100.0%; Pred. No. 1.6e-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 60
 Db 1268 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 1327
 QY 61 GCCTAGTTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 120
 Db 1328 GCCTAGTTTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 1387

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QY 121 AAGTCCTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
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Db 1388 AAGTCCTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1447
|||||
QY 181 AAATGAGCAAAATAT 194
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Db 1448 AAATGAGCAAAATAT 1461

RESULT 4
HUMIL1
LOCUS Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
DEFINITION Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
ACCESSION K02770
VERSION K02770.1 GI:186268
KEYWORDS Human endotoxin-stimulated monocyte, cDNA to mRNA, clones pA-26,
SOURCE pcD-415 and pcD-1218.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Webb,A.C., Webb,A.C., Rosenwasser,L.J., Mucci,S.F., Rich,A.,
Wolff,S.M. and Dinarello,C.A.
TITLE Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7907-7911 (1984)
MEDLINE 85088517
PUBMED 6083565
COMMENT A potential poly-A signal is found at position 1484-1489. Two
basic sequences that could be sites for protein processing, similar
to those observed for peptide hormones, are found at positions
708-716 and 723-728.
FEATURES
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/db_xref="taxon:9606"
<1..1496
/product="IL-1 mRNA"
87..896
/notes="interleukin 1 precursor polypeptide"
/codon_start=1
/protein_id="AAA36106.1"
/db_xref="GI:307043"
/translation="MAEVPKLASEMAYVSGNEDLLFFEADGPKQMKCFQDLDLCPL
DGGIQLRISDHHYKGFQAAVAVVAMDKRLKLVPCPTFOENDLSTFFPFIFEEEP
IFPDTWDAAYVHDAPVRSNCTLRDSQKSLVMSGPKYELKALHLOGDMEQGVFSM
SFVQGESNDKIPIVALGLKELNLYLSCVLKDDKPTQLQESVDPKNYPKKMKERFVN
KIEINNKLEFSAQFPNHYISTQAEENMPVFLGGTKGGQDITDFTMQFVSS"
BASE COUNT 416 a 361 c 328 g 391 t
ORIGIN
104 bp upstream of Alu site.
Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATGCTCTAATTTATCAAGGGGGCAAGAGTAGCAGTCTGTGTAAGA 60
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Db 1269 TTTTGATTCATGCTCTAATTTATCAAGGGGGCAAGAGTAGCAGTCTGTGTAAGA 1328
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QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATC 120
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Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATC 1388
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QY 121 AAGTCCTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
|||||
Db 1389 AAGTCCTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1448
|||||
QY 181 AAATGAGCAAAATAT 194
|||||
Db 1449 AAATGAGCAAAATAT 1462

RESULT 5
HUMIL1
LOCUS Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
DEFINITION Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
ACCESSION K02770
VERSION K02770.1 GI:186268
KEYWORDS Human endotoxin-stimulated monocyte, cDNA to mRNA, clones pA-26,
SOURCE pcD-415 and pcD-1218.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Webb,A.C., Webb,A.C., Rosenwasser,L.J., Mucci,S.F., Rich,A.,
Wolff,S.M. and Dinarello,C.A.
TITLE Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7907-7911 (1984)
MEDLINE 85088517
PUBMED 6083565
COMMENT A potential poly-A signal is found at position 1484-1489. Two
basic sequences that could be sites for protein processing, similar
to those observed for peptide hormones, are found at positions
708-716 and 723-728.
FEATURES
source Location/Qualifiers
1..1496
/organism="Homo sapiens"
/db_xref="taxon:9606"
<1..1496
/product="IL-1 mRNA"
87..896
/notes="interleukin 1 precursor polypeptide"
/codon_start=1
/protein_id="AAA36106.1"
/db_xref="GI:307043"
/translation="MAEVPKLASEMAYVSGNEDLLFFEADGPKQMKCFQDLDLCPL
DGGIQLRISDHHYKGFQAAVAVVAMDKRLKLVPCPTFOENDLSTFFPFIFEEEP
IFPDTWDAAYVHDAPVRSNCTLRDSQKSLVMSGPKYELKALHLOGDMEQGVFSM
SFVQGESNDKIPIVALGLKELNLYLSCVLKDDKPTQLQESVDPKNYPKKMKERFVN
KIEINNKLEFSAQFPNHYISTQAEENMPVFLGGTKGGQDITDFTMQFVSS"
BASE COUNT 416 a 361 c 328 g 391 t
ORIGIN
104 bp upstream of Alu site.
Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATGCTCTAATTTATCAAGGGGGCAAGAGTAGCAGTCTGTGTAAGA 60
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Db 1269 TTTTGATTCATGCTCTAATTTATCAAGGGGGCAAGAGTAGCAGTCTGTGTAAGA 1328
|||||
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATC 120
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Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATC 1388
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|||||
Db 1389 AAGTCCTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1448
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QY 181 AAATGAGCAAAATAT 194
|||||
Db 1449 AAATGAGCAAAATAT 1462

RESULT 5
HUMIL1C
LOCUS Human monocyte interleukin mRNA, complete cds.
DEFINITION Human monocyte interleukin mRNA, complete cds.
ACCESSION M54933
VERSION M54933.1 GI:186287
KEYWORDS interleukin 1.
SOURCE Human monocyte, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Webb,A.C., Dinarello,C.A., Rosenwasser,L.J., Mucci,S.F., Rich,A.,
Wolff,S.M. and Auron,P.E.
TITLE Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
JOURNAL Adv. Gene Technol. 22, 339-340 (1985)
FEATURES
source Location/Qualifiers
1..1496
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2ql2-q21"
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1..1496
/gene="IL1A"
1..1496
/gene="IL1A"
/notes="interleukin 1 mRNA; G00-120-695"
88..897
/gene="IL1A"
/notes="precursor protein"
/codon_start=1
/product="interleukin 1"
/protein_id="AAA59136.1"
/db_xref="GI:186288"
/db_xref="GDB:G00-120-695"
/translation="MAEVPKLASEMAYVSGNEHDLFFEADGPKQMKCFQDLDLCPL
DGGIQLRISDHHYKGFQAAVAVVAMDKRLKLVPCPTFOENDLSTFFPFIFEEEP
IFPDTWDAAYVHDAPVRSNCTLRDSQKSLVMSGPKYELKALHLOGDMEQGVFSM
SFVQGESNDKIPIVALGLKELNLYLSCVLKDDKPTQLQESVDPKNYPKKMKERFVN
KIEINNKLEFSAQFPNHYISTQAEENMPVFLGGTKGGQDITDFTMQFVSS"
BASE COUNT 416 a 367 c 322 g 391 t
ORIGIN
Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATGCTCTAATTTATCAAGGGGGCAAGAGTAGCAGTCTGTGTAAGA 60
|||||
Db 1269 TTTTGATTCATGCTCTAATTTATCAAGGGGGCAAGAGTAGCAGTCTGTGTAAGA 1328
|||||
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATC 120
|||||
Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATC 1388
|||||
QY 121 AAGTCCTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
|||||
Db 1389 AAGTCCTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1448
|||||
QY 181 AAATGAGCAAAATAT 194
|||||
Db 1449 AAATGAGCAAAATAT 1462

RESULT 6
E00846
LOCUS cDNA sequence for human IL-1.
DEFINITION cDNA sequence for human IL-1.
ACCESSION E00846
VERSION E00846.1 GI:2169107
KEYWORDS JP 19861191-A/1.
SOURCE unidentified.
ORGANISM unclassified.

```

REFERENCE 1 (bases 1 to 1507)
AUTHORS Shiratsugu, I.A., Chiyayasu, E.D., Andoriyyu, S.U., Arekisandaa, R.,
Shierudon, E.U., Rii, G. and Rani, J.R.
TITLE HUMAN IL-1CDNA HAVING BIOLOGICALLY ACTIVE HUMAN IL-1 PROTEINCODE
JOURNAL Patent: JP 19861191-A 1 06-JUN-1986;
MASSACHUSETTS INST OF TECHNOLOG <MIT>, NEW INGUANDO MEDICAL CENTER
HOSUPITARUZI INC. TRUSTEES OBU TAFUTSU KARETSUJI, UERESUREI
KARETSUJI
COMMENT OS Human {Homo sapiens}
PN JP 19861191-A/1
PD 06-JUN-1986
PF 18-MAY-1985 JP 1985104978
PR 18-MAY-1984 US 84 611669, 11-FEB-1985 US 85 700374 PI
FUIRITSUPU II AURON, CHIYAARUSU EE DEINARERO, PI ANDORIYU SHII
UEBU,
PI AREKISANDAA RITSUCHI, SHIERUDON EMU UORUFU, RII GEERUKE, PI
RANII JIEE ROZENWATSUSA
PC C12N15/00, A61K39/395, C07K13/00, C12N1/00, C12N5/00, C12P21/02, PC
(C12N1/00,
PC C12R1:19), (C12P21/02, C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=Blood;
CC *source: cell_type=Monocyte;
FH Key Location/Qualifiers
FT 5'UTR 1..86
FT CDS 87..896
FT /product='human IL-1'
FT mat_peptide 534..893
FT /product='peptide with human IL-1 activity' FT
FT mat_peptide 534..710
FT /product='peptide with human IL-1 activity' FT
FT mat_peptide 711..893
FT /product='peptide with human IL-1 activity' FT
FT 3'UTR 894..1507
FT polyA_signal 1484..1489.
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Location/Qualifiers
1..1507
/organism='unidentified'
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATTGGTCTTAATTTATTCAGAGGGGCAAGTAGCAGTGTCTGTAAGA 60
DB 1269 TTTTGATTCATTGGTCTTAATTTATTCAGAGGGGCAAGTAGCAGTGTCTGTAAGA 1328
QY 61 GCCTAGTTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 120
DB 1329 GCCTAGTTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 1388
QY 121 AGTCCTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 180
DB 1389 AGTCCTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 1448
QY 181 AAATGAGCAATAT 194
DB 1449 AAATGAGCAATAT 1462
RESULT 7
LOCUS I07942 1507 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent EP 0161901.
ACCESSION I07942
VERSION I07942.1 GI:589345

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1507)
AUTHORS Auron, P.E., Webb, A.C., Gehrke, L., Dinarallo, C.A., Rosenwasser, L.J.,
Rich, A. and Wolff, S.M.
TITLE Human il-1 cDNA sequences encoding biologically-active human il-1
proteins
JOURNAL Patent: EP 0161901-A2 1 21-NOV-1985;
FEATURES
source
Location/Qualifiers
1..1507
/organism='unknown'
BASE COUNT 427 a 361 c 328 g 391 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATTGGTCTTAATTTATTCAGAGGGGCAAGTAGCAGTGTCTGTAAGA 60
DB 1269 TTTTGATTCATTGGTCTTAATTTATTCAGAGGGGCAAGTAGCAGTGTCTGTAAGA 1328
QY 61 GCCTAGTTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 120
DB 1329 GCCTAGTTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 1388
QY 121 AGTCCTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 180
DB 1389 AGTCCTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 1448
QY 181 AAATGAGCAATAT 194
DB 1449 AAATGAGCAATAT 1462
RESULT 8
LOCUS AX052806 9721 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 16 from Patent WO0071753.
ACCESSION AX052806
VERSION AX052806.1 GI:12226963
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9721)
AUTHORS Kornman, K.S., Duff, G.W., Crossman, D.C., Francis, S.E. and
Stephenson, K.
TITLE Diagnostics and therapeutics for restenosis
JOURNAL Patent: WO 0071753-A 16 30-NOV-2000;
FEATURES
source
Location/Qualifiers
1..9721
/organism='Homo sapiens'
/db_xref='taxon:9606'
/note='IL-1B gene-'n', bases throughout the sequence may be
A, T, C, G, other or unknown"
BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others
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Query Match 82.2%; Score 194; DB 6; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 8710 TTTTGATTCATTGGTCTTAATTTATTCAGAGGGGCAAGTAGCAGTGTCTGTAAGA 8769
QY 61 GCCTAGTTTTAATAGCTATGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 120

Db 8770 GCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGAGTGGTGTCTCTCTTTAAATC 8829

QY 121 AAGTCCCTTTAATTAAGACTGAATATATATAGCTCAGATTATTAAATGGGAATATTAT 180

Db 8830 AAGTCCCTTTAATTAAGACTGAATATATATAGCTCAGATTATTAAATGGGAATATTAT 8889

QY 181 AAATGAGCAAAATAT 194

Db 8890 AAATGAGCAAAATAT 8903

RESULT 9

AX067266

LOCUS

DEFINITION

AX067266

ACCESSION

AX067266

VERSION

AX067266.1

KEYWORDS

GI:12544890

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 9721)

AUTHORS

Duff,G.W., Cox,A., Camp,N.J. and di Giovine,F.S.

TITLE

Diagnosics and therapeutics for diseases associated with an il-1 inflammatory haplotype

JOURNAL

Patent: WO 0100880-A 2 04-JAN-2001;

Interleukin Genetics, Inc. (US)

FEATURES

source

1..9721

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT

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ORIGIN

Query Match 82.2%; Score 194; DB 6; Length 9721;

Best Local Similarity 100.0%; Pred. No. 1.2e-86;

Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTCTTCTTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60

Db 8710 TTTTGATTCTTCTTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGA 8769

QY 61 GCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGAGTGGTGTCTCTTTAAATC 120

Db 8770 GCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGAGTGGTGTCTCTTTAAATC 8829

QY 121 AAGTCCCTTTAATTAAGACTGAATATATATAGCTCAGATTATTAAATGGGAATATTAT 180

Db 8830 AAGTCCCTTTAATTAAGACTGAATATATATAGCTCAGATTATTAAATGGGAATATTAT 8889

QY 181 AAATGAGCAAAATAT 194

Db 8890 AAATGAGCAAAATAT 8903

RESULT 11

HS111B

LOCUS

DEFINITION

Human gene for prointerleukin 1 beta.

ACCESSION

X04500

VERSION

X04500.1

KEYWORDS

GI:33788

SOURCE

interleukin 1 beta.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 9721)

AUTHORS

Clark,B.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auron,P.E.

TITLE

Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene

JOURNAL

Nucleic Acids Res. 14 (20), 7897-7914 (1986)

MEDLINE

87040762

PUBMED

3490654

COMMENT

Data kindly reviewed (13-MAY-1988) by Clark B.D.

FEATURES

source

1..9721

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="2"

/map="ql3-q24"

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669..360

/note="Alu repeat"

1576..1581

/note="TATA-box like sequence"

1809..1816

CAAT_signal

1859..1866

CAAT_signal

1903..1909

TATA_signal

1934..1935

prim_transcript

1934..2005

exon

/number=1

misc_feature

complement(1936..1943)

misc_feature

/note="pot. viral enhancer core sequence"

2006..2465

intron

/number=1

repeat_region

2039..2055

/note="direct repeat 2"

2291..2297

misc_feature

/note="pot. viral enhancer core sequence"

INSTITUTE, INC. (US)

Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

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ORIGIN

Query Match 82.2%; Score 194; DB 6; Length 9721;

Best Local Similarity 100.0%; Pred. No. 1.2e-86;

Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTCTTCTTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60

Db 8710 TTTTGATTCTTCTTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGA 8769

QY 61 GCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGAGTGGTGTCTCTTTAAATC 120

Db 8770 GCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGAGTGGTGTCTCTTTAAATC 8829

QY 121 AAGTCCCTTTAATTAAGACTGAATATATATAGCTCAGATTATTAAATGGGAATATTAT 180

Db 8830 AAGTCCCTTTAATTAAGACTGAATATATATAGCTCAGATTATTAAATGGGAATATTAT 8889

QY 181 AAATGAGCAAAATAT 194

Db 8890 AAATGAGCAAAATAT 8903

RESULT 11

HS111B

LOCUS

DEFINITION

Human gene for prointerleukin 1 beta.

ACCESSION

X04500

VERSION

X04500.1

KEYWORDS

GI:33788

SOURCE

interleukin 1 beta.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 9721)

AUTHORS

Clark,B.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auron,P.E.

TITLE

Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene

JOURNAL

Nucleic Acids Res. 14 (20), 7897-7914 (1986)

MEDLINE

87040762

PUBMED

3490654

COMMENT

Data kindly reviewed (13-MAY-1988) by Clark B.D.

FEATURES

source

1..9721

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/db_xref="taxon:9606"

/chromosome="2"

/map="ql3-q24"

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1576..1581

/note="TATA-box like sequence"

1809..1816

CAAT_signal

1859..1866

CAAT_signal

1903..1909

TATA_signal

1934..1935

prim_transcript

1934..2005

exon

/number=1

misc_feature

complement(1936..1943)

misc_feature

/note="pot. viral enhancer core sequence"

2006..2465

intron

/number=1

repeat_region

2039..2055

/note="direct repeat 2"

2291..2297

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/note="pot. viral enhancer core sequence"

misc_feature 2458..2465
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/protein_id="CA28185.1"
/db_xref="GI:312408"
/db_xref="Swiss-Prot:PO1584"
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IFDVTWNEAVVADAPVRSNCLTRDSQOKSLVMSGPEYELKALHLOGQDMEQVVPFSM
SFVQGESRDNKI PVALGKEKNLYLSCVLKDKDKPTQLQESVDEKPKKMKRFFVN
KIEINNKLEFESAQFPNNYISTQAENMPVFLGTTGGQDIDFTWQFVSS"
2528..3091
/number=2
complement(2714..2721)
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2858..2865
/note="pot.viral enhancer core sequence"
3092..3143
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3144..5124
/number=3
4266..4273
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4274..4279
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5125..5326
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5327..5873
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5489..5497
/note="pot.viral enhancer core sequence"
5874..6038
/number=5
6039..7274
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6205..6212
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6213..6220
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complement(6910..6915)
/note="pot.viral enhancer core sequence"
complement(6916..6924)
/note="pot.viral enhancer core sequence"
complement(7247..7253)
/note="pot.viral enhancer core sequence"
7275..7405
/number=6
7406..8126
/number=6
7413..7426
/note="pot. viral enhancer core sequence"
8127..8953
/number=7
8925..8930
/note="pot polyA signal"
8953
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9331..9721
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/number=2661 a 2328 c 2122 g 2608 t 2 others
BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN
Query Match 82.2%; Score 194; DB 9; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATTGGTCTAAATTATTCAAAGGGGCAAGTAGCAGTGTCTGTAAGA 60

Db 8710 TTTTGATTCATTGGTCTAAATTATTCAAAGGGGCAAGTAGCAGTGTCTGTAAGA 8769
QY 61 GCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACGTGGTGTCTCTTTAAATC 120
Db 8770 GCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACGTGGTGTCTCTTTAAATC 8829
QY 121 AAGTCTTTTAATAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTAT 180
Db 8830 AAGTCTTTTAATAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTAT 8889
QY 181 AATGAGCAATAT 194
Db 8890 AATGAGCAATAT 8903
RESULT 12
AX419978 1382 bp mRNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 315 from Patent WO0198537.
ACCESSION AX419978
VERSION AX419978.1 GI:21524345
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 315 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
Location/Qualifiers
1..1382
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 380 a 334 c 308 g 360 t
ORIGIN
Query Match 80.1%; Score 189; DB 6; Length 1382;
Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAAATTATTCAAAGGGGCAAGTAGCAGTGTCTGTAAGAAGCCTA 65
Db 1183 ATTCATTGGTCTAAATTATTCAAAGGGGCAAGTAGCAGTGTCTGTAAGAAGCCTA 1242
QY 66 GTTTTAAATAGCTATGGAATCAATTCAATTGGACGTGGTGTCTCTTTAAATCAAGTC 125
Db 1243 GTTTTAAATAGCTATGGAATCAATTCAATTGGACGTGGTGTCTCTTTAAATCAAGTC 1302
QY 126 CTTTAAATAGCTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
Db 1303 CTTTAAATAGCTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 1362
QY 186 AGCAATAT 194
Db 1363 AGCAATAT 1371
RESULT 13
HSPRO11B 1473 bp mRNA linear PRI 06-DEC-1990
LOCUS
DEFINITION Human mRNA for prointerleukin 1 beta.
ACCESSION X56087
VERSION X56087.1 GI:35662
KEYWORDS prointerleukin 1; prointerleukin 1 beta.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Kotenko,S.V., Buleikov,M.T., Veiko,V.P., Epishin,S.M.,

Lomakin, I. B., Kurbatova, A. V., Kozlov, A. P., Konusova, V. G., Kotov, A. V., Erel, T. V., Reshetnikov, V. L., Simbitsev, A. S., Kettinglii, S. A. and Vinetskiy, Y. P.
Cloning of the cDNA coding for human interleukin-1 alpha and interleukin-1 beta
Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989)
JOURNAL
90249285
MEDLINE
2635664
PUBMED

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FEATURES             Location/Qualifiers
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BASE COUNT
ORIGIN

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QY	126	CTTTTAATTTAAGACGTGAAAATATATAGCTCAGATTATTTAAATCGGAATATTTTATAAATG	185	
DB	1362	CTTTTAATTTAAGACGTGAAAATATATAGCTCAGATTATTTAAATCGGAATATTTTATAAATG	1421	
QY	186	AGCAAATAT	194	
DB	1422	AGCAAATAT	1430	

RESULT 14					
AR030386					
LOCUS			1497 bp	DNA	linear
DEFINITION			Sequence 10 from patent US 5861267.		
ACCESSION			AF030386		
VERSION			AF030386.1		
KEYWORDS			GI:5943600		
SOURCE			Unknown.		
ORGANISM			Unknown.		
REFERENCE			Unclassified.		
AUTHORS			1 (bases 1 to 1497)		
TITLE			Su, W.		
JOURNAL			Methods, nucleotide sequences and host cells for assaying exogenous		
FEATURES			and endogenous protease activity		
source			Patent: US 5861267-A 10 19-JAN-1999;		
			Location/Qualifiers		
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Best Local Similarity	100.0%; Pred.No.5.2e-84;				
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Qy	6	ATTTCATTGGTCTAATTTATTTCAAAGGGGGCGAAGAAGTAGCAGTGTCTGTGTAAAGAGCCTA	65		
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Qy	126	CTTTAAATAGACTGAAATATATTAAGCTCAGATATTTAAATCGGATATTTTAAATG	185		
Db	1391	CTTTAAATAGACTGAAATATATTAAGCTCAGATATTTAAATCGGATATTTTAAATG	1450		
Qy	186	AGCAAAATAT	194		
Db	1451	AGCAAAATAT	1459		
RESULT 15					
E06734	LOCUS E06734 1497 bp RNA linear PAT 29-SEP-1997				
DEFINITION	DNA encoding IL-1 beta.				
ACCESSION	E06734				
VERSION	E06734.1 GI:2174916				
KEYWORDS	JP 1994041185-A/5.				
SOURCE	Unidentified.				
ORGANISM	synthetic construct.				
REFERENCE	1. (bases 1 to 1497)				
AUTHORS	Higaki, M., Shoji, Y. and Mizushima, Y.				
TITLE	ONOSPHOOLIGONUCLEOTIDE AND ITS USE				
JOURNAL	Patent: JP 1994041185-A 5 15-FEB-1994;				
COMMENT	L T T KENKYUSHO:KK JP 1994041185-A/5 PD 15-FEB-1994 PZ 16-JUL-1992 JP 199213519 PI HIGAKI MEGUMI, SHOJI YOKO, MIZUSHIMA YUTAKA PC C07H21/04,A61K31/70,A61K31/70.C12P19/34; CC strandedness: Double; CC topology: Linear; FH Key Location/Qualifiers PH FT mat_peptide 1..1497 FT /product='IL-1 beta'. FT Location/Qualifiers 1..1497 /organism="synthetic construct" /db_xref="taxon:32630"				
FEATURES					
source					
BASE COUNT	411 a	365 c	331 g	390 t	
ORIGIN					

	Query Match	80.1%	Score 189	DB 6	Length 1497	
	Best Local Similarity	100.0%	Prod. NO. 5.2e-84			
	Matches 189	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
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Db	1271	ATTCAATTGGTCTAATTTATTTCAAAAGGGGGCAAGAAGTAGCAGTCTCTGTAAAGAGCCTA	1330			
Qy	66	GTTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTGCTCTCTTTAAATCAAGTC	125			
Db	1331	GTTTTTAAAGCTATGGAATCAATTCAATTGGACTGGTGTGCTCTCTTTAAATCAAGTC	1390			
Qy	126	CTTTAAATTAAGACTGAAAAATATAATPAAGCTCAGATTATTTAAATCGGGAATATTTTATAAATG	185			
Db	1391	CTTTAAATTAAGACTGAAAAATATAATPAAGCTCAGATTATTTAAATCGGGAATATTTTATAAATG	1450			

Oy 186 AGCAATAT 194
|||
Db 1451 AGCAATAT 1459

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Job time : 1157 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 19:52:45 ; Search time 224 Seconds
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2372.641 Million cell updates/sec

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	236	100.0	9721	21	AAA50175 Human interleukin-
2	194	82.2	656	21	AAA51659 Interleukin 1-beta
3	194	82.2	1496	21	AA220946 Human interleukin-
4	194	82.2	1496	21	AAA34824 Human adenosine re
5	194	82.2	1507	6	AA250060 Sequence encoding
6	194	82.2	1507	14	AAQ50981 Human interleukin-
7	194	82.2	9721	20	AAQ75924 Human interleukin-
8	194	82.2	9721	21	AA220945 Human interleukin-
9	194	82.2	9721	21	AAC63768 Human IL-1B gene.

10	194	82.2	9721	21	AAA50174 Human interleukin-
11	194	82.2	9721	21	AAA34823 Human adenosine re
12	194	82.2	9721	22	AA227666 IL-1B DNA. Uniden
13	194	82.2	9721	22	AA2291434 Human IL-1B nucleo
14	194	82.2	9721	24	AA235192 Human prointerleuk
15	194	82.2	29433	21	AA220950 Human interleukin-
16	194	82.2	29433	21	AAA34828 Human adenosine re
17	194	82.2	209273	21	AA221437 Human factor-relat
18	194	82.2	1382	24	ABL46348 Human interleukin-
19	194	80.1	1497	21	AA220944 Human interleukin-
20	194	80.1	1497	21	AA220944 Human adenosine re
21	194	80.1	1497	21	AA220944 Human CDNA differe
22	194	80.1	1497	24	AA220944 Human IL1B gene.
23	194	80.1	7824	22	AA224368 Human interleukin-
24	194	80.1	7824	24	AA224368 Human interleukin
25	194	80.1	7824	24	AA224368 Human IL-1ra BAC c
26	194	80.1	14690	20	AA222303 IL-1 beta gene.
27	194	80.1	14690	20	AA222303 cDNA encoding huma
28	194	80.1	14690	20	AA222303 Human gene signatu
29	194	80.1	14690	20	AA222303 Sequence encoding
30	194	80.1	14690	20	AA222303 Human interleukin-
31	194	80.1	14690	20	AA222303 Human spliced tran
32	194	80.1	14690	20	AA222303 Probe used to dete
33	194	80.1	14690	20	AA222303 Monkey IL-2 beta g
34	194	80.1	14690	20	AA222303 Human IL-1ra BAC c
35	194	80.1	14690	20	AA222303 Probe used to dete
36	194	80.1	14690	20	AA222303 Probe used to dete
37	194	80.1	14690	20	AA222303 Probe used to dete
38	194	80.1	14690	20	AA222303 Probe used to dete
39	194	80.1	14690	20	AA222303 Probe used to dete
40	194	80.1	14690	20	AA222303 Probe used to dete
41	194	80.1	14690	20	AA222303 Probe used to dete
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44	194	80.1	14690	20	AA222303 Probe used to dete
45	194	80.1	14690	20	AA222303 Probe used to dete

ALIGNMENTS

RESULT 1	AAA50175	AAA50175 standard; DNA; 9721 BP.
ID	AAA50175	standard; DNA; 9721 BP.
XX	XX	AAA50175;
AC	AC	AAA50175;
DT	DT	07-NOV-2000 (first entry)
XX	XX	Human interleukin-1 beta allele 2 (+6912).
DE	DE	Human interleukin-1 beta; IL-1B; human; polymorphism; inflammation;
XX	XX	coronary artery disease; osteoporosis; nephropathy;
KW	KW	alopecia areata; Graves disease; systemic lupus erythematosus;
KW	KW	lichen sclerosus; ulcerative colitis; diabetic retinopathy;
KW	KW	periodontal disease; juvenile chronic arthritis; psoriasis;
KW	KW	insulin dependent diabetes; asthma; lung fibrosis;
KW	KW	chronic inflammatory liver disease; rheumatoid arthritis;
KW	KW	chronic inflammatory lung disease; antiinflammatory; osteopathic;
KW	KW	dermatological; immunosuppressive; antidiabetic; antithyroid;
KW	KW	antiarthritic; antirheumatic; antiasthmatic; antipsoriatic;
KW	KW	hepatotropic; antiulcer; diagnosis; therapy; ds.
OS	OS	Homo sapiens.
XX	XX	Location/Qualifiers
PH	PH	Key
FT	FT	Variation
FT	FT	replace(8904,C)
FT	FT	/*tag= a
XX	XX	/note= "IL-1B allele 2 (+6912)"
PN	PN	WO200047619-A1.
XX	XX	17-AUG-2000.
PD	PD	

XX PF 10-FEB-2000; 2000WO-US03443.
XX DE 10-FEB-1999; 99US-0247874.
XX PR (INTE-) INTERLEUKIN GENETICS INC.
XX PA Duff GW, Di Giovine FS;
XX PI WPI; 2000-558192/51.
XX DR Novel methods and nucleic acids for diagnosing and treating disorders
XX PT associated with high levels of interleukin 1beta, especially
XX PT inflammatory diseases -
XX PS Claim 34; Fig 2; 74pp; English.
XX CC The present sequence is that of human interleukin-1 beta (IL-1B)
XX CC allele 2 (+6912), which is a form of the IL-1B gene that contains
XX CC guanine at position +6912; IL-1B allele 1 (+6912) has cytosine at
XX CC this position (see AA50174). The invention is based on the
XX CC identification of this novel allele at marker +6912 of the IL-1B
XX CC gene. The C to G transition occurs within the 3' untranslated
XX CC region of the IL-1B gene and results in an increased level of IL-1B
XX CC protein. Individuals homozygous for the IL-1B allele 2 (+6912)
XX CC accumulate approximately 4 times more immunoreactive IL-1B protein
XX CC than homozygotes for IL-1B allele 1 (+6912). Methods and kits are
XX CC provided for detecting IL-1B allele 2 (+6912), or an allele in
XX CC linkage disequilibrium with an IL-1B allele 2 (+6912), and
XX CC thereby determining a patient's susceptibility to developing
XX CC inflammatory disorders, especially coronary artery disease,
XX CC osteoporosis, nephropathy in diabetes mellitus, alopecia areata,
XX CC Graves disease, systemic lupus erythematosus, lichen sclerosis,
XX CC ulcerative colitis, diabetic retinopathy, periodontal disease,
XX CC juvenile chronic arthritis, psoriasis, insulin dependent diabetes,
XX CC asthma, chronic inflammatory liver disease, chronic inflammatory
XX CC lung disease, lung fibrosis, and rheumatoid arthritis (claimed).
XX CC Identification of the IL-1B allele 2 (+6912) and its involvement in
XX CC IL-1B overproduction also enables screening assays for identifying
XX CC IL-1B antagonists that can be used to treat conditions associated
XX CC with IL-1B allele 2 (+6912). Transgenic animals are also claimed,
XX CC and can be used to identify IL-1B agonists and antagonists, or
XX CC to confirm the safety and efficacy of candidate therapeutics.
XX SQ Sequence 9721 BP; 2661 A; 2327 C; 2123 G; 2608 T; 2 other;
Query Match 100.0%; Score 236; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATTGGTCTTAATTTTCAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 60
DB 8710 TTTTGATTCATTGGTCTTAATTTTCAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 8769
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGAGCTGGTGTCTCTTTAAATC 120
DB 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGAGCTGGTGTCTCTTTAAATC 8829
QY 121 AAGTCCTTTTAATAGCTGAAATATATAAGCTCAGATTTTAAATGGGAATTTTAT 180
DB 8830 AAGTCCTTTTAATAGCTGAAATATATAAGCTCAGATTTTAAATGGGAATTTTAT 8889
QY 181 AAATGAGCAAAATATGATACCTGTTCAATGGTTCTGAAATTAACCTTCACCTGAAGAAA 236
DB 8890 AAATGAGCAAAATATGATACCTGTTCAATGGTTCTGAAATTAACCTTCACCTGAAGAAA 8945
RESULT 2
ID AA51659
XX AA51659 standard; cDNA; 656 BP.
AC AA51659;
XX

DT 31-OCT-2000 (first entry)
XX XX Interleukin 1-beta 3' UTR cDNA.
XX KW IL-1-beta; 3' UTR; interleukin 1-beta; AU-rich element; ARE motif;
XX KW mRNA instability; rheumatoid arthritis; osteoarthritis; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT repeat_region 404..416
FT /tag= a
FT /rpt_type= TANDEM
FT /note= "3 copies of AU-rich motif"
FT repeat_unit 404..408
FT /tag= b
FT /note= "AU-rich motif"
FT misc_feature 406..414
FT /tag= c
FT polyA_signal 644..649
FT /note= "Minimal instability motif"
FT /tag= d
PN WO200039314-A1.
XX 06-JUL-2000.
XX 23-DEC-1999; 99WO-CA01235.
XX 24-DEC-1998; 98GB-0028709.
XX (NOVA-) NOVATION PHARM INC.
XX Kastelic T, Cheneval D;
XX WPI; 2000-452406/39.
XX Identifying compounds which affect mRNA stability for the treatment of
XX disease e.g. arthritis comprises a DNA expression system expressing a
XX protein having a detectable signal
XX Disclosure; Fig 1; 31pp; English.
XX This is the 3' UTR of interleukin 1-beta mRNA which contains AU-rich
XX element (ARE) motifs. These ARE motifs are found in genes subject to
XX mRNA instability. Identification of a compound which affects mRNA
XX stability comprises a DNA expression system which in the absence of the
XX test compound is capable of expressing a protein having a detectable
XX signal. The mRNA which codes for the protein, and which is transcribed
XX from the expression system, comprises at least one copy of a mRNA
XX instability sequence. The mRNA is contacted with a test compound and
XX the detectable signal is measured in the presence of the test compound
XX and compared with a control. Compounds identified by the new method can
XX be used for the treatment of a disease or medical condition which
XX involves inappropriate mRNA stabilization and/or accumulation and
XX undesirable protein expression (claimed) e.g. rheumatoid arthritis or
XX osteoarthritis.
XX SQ Sequence 656 BP; 176 A; 151 C; 129 G; 200 T; 0 other;
Query Match 82.2%; Score 194; DB 21; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATTGGTCTTAATTTTCAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 60
DB 429 TTTTGATTCATTGGTCTTAATTTTCAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 488
QY 61 GCCTAGTTTTTAATAGCTGAAATATATAAGCTCAGATTTTAAATGGGAATTTTAT 120
DB 489 GCCTAGTTTTTAATAGCTGAAATATATAAGCTCAGATTTTAAATGGGAATTTTAT 548
QY 121 AAGTCCTTTTAATAGCTGAAATATATAAGCTCAGATTTTAAATGGGAATTTTAT 180

Db 549 AAGCCCTTAAATAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 608
QY 181 AAATGAGCAATAT 194
Db 609 AAATGAGCAATAT 622

RESULT 3
ID AAF20946 standard; DNA; 1496 BP.
XX AC AAF20946;
XX 14-MAR-2001 (first entry)
XX Human interleukin-1 polynucleotide fragment #2513.
DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX Homo sapiens.
XX OS
XX PN WO200062736-A2.
XX PD 26-OCT-2000.
XX 24-MAR-2000; 2000WO-US08020.
XX 06-APR-1999; 99US-0127958.
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX Nyce JW;
XX WPI; 2000-679539/66.
XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX Disclosure; Page 232-233; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, defensins, growth factors, vasoactive peptides and
CC transmitters, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
XX the present invention.

SQ Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;
Query Match 82.2%; Score 194; DB 21; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1269 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAGA 1328
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTCTCTTTAAATC 120
Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTCTCTTTAAATC 1388
QY 121 AAGTCCTTTTAATAGCTGAAATATATAAGCTCAGATTATTAAATGGGAATTTAT 180
Db 1389 AAGTCCTTTTAATAGCTGAAATATATAAGCTCAGATTATTAAATGGGAATTTAT 1448
QY 181 AAATGAGCAATAT 194
Db 1449 AAATGAGCAATAT 1462

RESULT 4
ID AAA34824 standard; DNA; 1496 BP.
XX AC AAA34824;
XX 28-JUL-2000 (first entry)
XX Human adenosine receptor related polynucleotide SEQ ID NO:2513.
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
XX OS
XX PN WO200009525-A2.
XX 24-FEB-2000.
XX 03-AUG-1999; 99WO-US17712.
XX 03-AUG-1998; 98US-0095212.
XX (UYEC-) UNIV EAST CAROLINA.
XX Nyce JW;
XX WPI; 2000-205971/18.
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypercension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX Disclosure; Page 675; 1343pp; English.

XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AA32313 to AA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AA32323 to AA33992) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;

Query Match 82.2%; Score 194; DB 21; Length 1496;
 Best Local Similarity 100.0%; Pred. No. 1.3e-85;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTGATTGCTGCTAATTTAATTCAAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 60
 Db 1269 TTTTGATTGCTGCTAATTTAATTCAAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 1328
 QY 61 GCCTAGTTTTTAATGACTATGGAATCAATTCATTTGGACTGGTGTCTCTTAATC 120
 Db 1329 GCCTAGTTTTTAATGACTATGGAATCAATTCATTTGGACTGGTGTCTCTTAATC 1388
 QY 121 AAGTCCTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
 Db 1389 AAGTCCTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1448
 QY 181 AAATGAGCAAAATAT 194
 Db 1449 AAATGAGCAAAATAT 1462

RESULT 5
 AA50060
 ID AA50060 standard; cDNA; 1507 BP.

AC AA50060;

DT 09-SEP-1991 (first entry)

XX Sequence encoding interleukin-1 (IL-1).

XX Immunological reagent; T cell stimulant; B cell; immunoglobulin; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 87..894
 XX /*tag= a

XX EP161901-A.

XX 21-OCT-1985.

XX 07-MAY-1985; 85EP-0303234.

XX 11-FEB-1985; 85US-0700374.
 PR (NEW) NEW ENGLAND MED CEN.
 XX Auron PE, Webb AC, Gehrke L, Dinarello CA, Rosenwasser LJ, Rich A;
 PI Wolff SW;
 XX WPI; 1985-291135/47.
 DR P-PSDB; AAP50043.
 XX Recombinant cloning vehicle contg. human interleukin-7 gene-or its
 PT fragments, producing new biologically active polypeptide(s)
 XX Claim 7; Page 34-35; 39pp; English.
 XX A pure cDNA of 1507 bp (AA50060) (and its 1-606, 1-677, 1355-1507;
 CC 482-1501; 482-677; and 1355-1507 fragments) are claimed. Also
 CC claimed is a recombinant DNA cloning vehicle contg. the human IL-1
 CC gene sequence. Specifically the vehicle contains the sequence coding
 CC for the new 287 AA sequence (AAP50043) or the following new fragments
 CC (1) 9-224; (2) 1-210-X; (3) 144-287; and (4) 144-210-(X); (X= Asn-
 CC Ser-Ile-Trip-Thr-Gly-Val-Leu-Ser-Leu-Asn-Gln-Val-Leu).
 XX Sequence 1507 BP; 427 A; 361 C; 328 G; 391 T; 0 other;

Query Match 82.2%; Score 194; DB 6; Length 1507;
 Best Local Similarity 100.0%; Pred. No. 1.3e-85;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTGCTGCTAATTTAATTCAAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 60
 Db 1269 TTTTGATTGCTGCTAATTTAATTCAAAGGGGGGCAAGTAGCAGTGTCTGTAAGA 1328
 QY 61 GCCTAGTTTTTAATGACTATGGAATCAATTCATTTGGACTGGTGTCTCTTAATC 120
 Db 1329 GCCTAGTTTTTAATGACTATGGAATCAATTCATTTGGACTGGTGTCTCTTAATC 1388
 QY 121 AAGTCCTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
 Db 1389 AAGTCCTTTAATTAAGCTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1448
 QY 181 AAATGAGCAAAATAT 194
 Db 1449 AAATGAGCAAAATAT 1462

RESULT 6
 AAQ50981
 ID AAQ50981 standard; cDNA; 1507 BP.

AC AAQ50981;

DT 19-MAY-1994 (first entry)

XX Human Interleukin-1 coding sequence.

XX hIL-1; interleukin; cytokine; truncated; N-terminal deletion;

XX C-terminal deletion; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 87..896
 XX /*tag= a
 XX /product= hIL-1
 XX /note= "N- and C-terminally truncated forms of
 XX this sequence which retain IL-1 activity
 XX are covered by the invention"

XX EP569687-A.

XX 18-NOV-1993.


```
XX 07-MAY-1985; 85EP-0303234.
XX PF
XX 18-MAY-1984; 84US-0611669.
XX PR
XX 11-FEB-1985; 85US-0700374.
XX PR
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PA (NEW-) NEW ENGLAND MED. CENT HOSPITALS.
XX PA (TUFT ) TUFTS COLLEGE.
XX PA (WELL-) WELLESLEY COLLEGE.
XX PI Auron PE, Dinarello CA, Gehrke L, Rich A, Rosenwasser LJ;
XX PI Webb AC, Wolff SM;
XX DR
XX WPI; 1993-360975/46.
XX DR P-PSDB; AAR42213.
XX PT New DNA encoding protein with IL-1 activity - useful in
XX PT monitoring disease states e.g. cancer and studying inflammation
XX PT e.g. in arthritis etc.
XX PS Claim 1; Page 11-16; 24pp; English.
XX CC DNA comprising part of the nucleotide sequence AAQ50981 which encodes
XX CC a polypeptide having IL-1 activity and a mol.wt. of 20000 is claimed.
XX CC Specifically, the region between nucleotides 111-717 has been found
XX CC to retain hIL-1 activity (see AAQ45464).
XX SQ Sequence 1507 BP; 427 A; 361 C; 328 G; 391 T; 0 other;
Query Match 82.2%; Score 194; DB 14; Length 1507;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATTGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 60
Db 1269 TTTTGATTCATTGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 1328
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGAGCTGTGCTCTCTTTAAATC 120
Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGAGCTGTGCTCTCTTTAAATC 1388
QY 121 AAGTCCTTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 180
Db 1389 AAGTCCTTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 1448
QY 181 AAATGAGCAAAATAT 194
Db 1449 AAATGAGCAAAATAT 1462
RESULT 7
AAX75924
ID AAX75924 standard; DNA; 9721 BP.
XX AC
XX AAX75924;
XX DT 29-JUL-1999 (first entry)
XX DE Human interleukin 1B gene.
XX KW Human; interleukin 1; IL-1B; IL-1A; IL-1RN; diagnosis; detection;
XX KW chronic obstructive airway disease; chronic bronchitis; emphysema;
XX KW asthma; chronic bronchiolitis; proinflammatory haplotype; ss.
XX OS Homo sapiens.
XX PN MO9924615-A2.
XX PD 20-MAY-1999.
XX PF 09-NOV-1998; 98WO-US23721.
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PR 12-JAN-1998; 98US-0005923.
PR 07-NOV-1997; 97GB-0023553.
XX PA (MEDI-) MEDICAL SCI SYSTEMS INC.
XX PI Barnes PJ, Duff GW, Giovine M, Lim S;
XX DR WPI; 1999-327420/27.
XX PT Genotyping nucleic acid samples for interleukin-1 (IL-1)
XX PT proinflammatory haplotype alleles useful for predicting
XX PT susceptibility to developing chronic obstructive airway disease
XX PS Example 1; Fig 2; 37pp; English.
XX CC The present invention describes genotyping a nucleic acid sample from a
XX CC subject to determine at least one allele of an interleukin-1 (IL-1)
XX CC proinflammatory haplotype. A method has also been described for
XX CC determining a subject's susceptibility to developing chronic obstructive
XX CC airway disease (COAD) or for predicting the rapidity or ultimate
XX CC progression of a COAD in the subject by: (a) obtaining a nucleic acid
XX CC sample from the subject; and (b) detecting at least one allele of an
XX CC IL-1 proinflammatory haplotype in the sample, where detection of at
XX CC least one of these alleles indicates that the patient has an increased
XX CC susceptibility to developing COAD. The method is useful for determining
XX CC the susceptibility of subjects to developing chronic obstructive airway
XX CC disease or for predicting the rapidity or ultimate progression of
XX CC chronic obstructive airway disease (COAD). COAD can be asthma, emphysema,
XX CC chronic bronchitis or chronic bronchiolitis. The method provides for
XX CC early identification of chronic obstructive airway disease (COAD),
XX CC facilitating administration of appropriate treatment at the earliest
XX CC stage, thereby increasing the probability of a positive outcome. The
XX CC present sequence represents the human IL-1B gene.
XX SQ Sequence 9721 BP; 2662 A; 2328 C; 2121 G; 2608 T; 2 other;
Query Match 82.2%; Score 194; DB 20; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCATTGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 60
Db 8710 TTTTGATTCATTGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAGA 8769
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGAGCTGTGCTCTCTTTAAATC 120
Db 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGAGCTGTGCTCTCTTTAAATC 8829
QY 121 AAGTCCTTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 180
Db 8830 AAGTCCTTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 8889
QY 181 AAATGAGCAAAATAT 194
Db 8890 AAATGAGCAAAATAT 8903
RESULT 8
AAX20945
ID AAX20945 standard; DNA; 9721 BP.
XX AC
XX AAX20945;
XX DT 14-MAR-2001 (first entry)
XX DE Human interleukin-1 polynucleotide fragment #2512.
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX KW human; airway disorder; bronchoconstriction; lung inflammation;
XX KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX KW respiratory obstruction; pulmonary obstruction; impeded respiration;
XX KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
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respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

OS Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

XX 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

DR WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

XX Disclosure; Page 230-232; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAR18434 to AAR21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

Query Match 82.2%; Score 194; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTCATTGGTCTAATTTATTCAGAGGGGCGAAGAGTAGCAGTGTCTGTAAAGA 60
DB 8710 TTTTGATTCATTGGTCTAATTTATTCAGAGGGGCGAAGAGTAGCAGTGTCTGTAAAGA 8769

QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAATC 120

DB 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAATC 8829

QY 121 AAGTCCTTTTAATTAAGACTGAAAAATATAAAGCTCAGATTTATTTAATCGGAATTTAT 180

DB 8830 AAGTCCTTTTAATTAAGACTGAAAAATATAAAGCTCAGATTTATTTAATCGGAATTTAT 8889

QY 181 AAATGAGCAAAATAT 194

DB 8890 AAATGAGCAAAATAT 8903

RESULT 9

AAC63768

ID AAC63768 standard; DNA; 9721 BP.

XX AAC63768;

XX 08-FEB-2001 (first entry)

XX Human IL-1B gene.

XX Human; IL-1B; interleukin-1B; cytostatic; antiinflammatory;
XX immunosuppressive; dermatological; antimicrobial; antiarthritic;
XX IL-1 receptor antagonist; tumour necrosis factor alpha antagonist;
XX interstitial lung disease; interstitial pneumonia; pulmonary fibrosis;
XX rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;
XX systemic sclerosis; dermatomyositis; chromosome 2; ds.

XX Homo sapiens.

XX WO200060117-A2.

XX 12-OCT-2000.

XX 31-MAR-2000; 2000WO-US08492.

XX 02-APR-1999; 99US-0286108.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Duff GW, Di Giovine FS, Whyte M;

XX WPI; 2000-656234/63.

XX Method for predicting the risk of interstitial lung disease, comprising detecting an interleukin-1 receptor antagonist allele and tumor necrosis alpha allele or an allele in linkage disequilibrium with either of these alleles -

XX Claim 6; Fig 2; 102pp; English.

XX The present sequence is provided in a specification relating to a method for determining whether a subject has or is predisposed to develop an interstitial lung disease. The method involves detecting an interleukin-1 receptor antagonist (IL-1RN) (-2018) allele 2, a tumour necrosis alpha (TNF-A) (-308) allele 2, or an allele in linkage disequilibrium with either of these two alleles. The method may be used to determine whether a subject has or is predisposed to develop an interstitial pneumonia or a pulmonary fibrosis and other disorders such as rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, systemic sclerosis, dermatomyositis. The method is also used for identifying molecules which can be used as therapeutics for treating interstitial lung disease.

XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

Query Match 82.2%; Score 194; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTCATTGGTCTAATTTATTCAGAGGGGCGAAGAGTAGCAGTGTCTGTAAAGA 60
DB 8710 TTTTGATTCATTGGTCTAATTTATTCAGAGGGGCGAAGAGTAGCAGTGTCTGTAAAGA 8769

QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAATC 120

DB 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAATC 8829

QY 121 AAGTCCTTTAAATTAAGACTCAAAATATATAAGCTCAGATTATTAAATGGGAATTTAT 180
 DB 8830 AAGTCCTTTAAATTAAGACTCAAAATATATAAGCTCAGATTATTAAATGGGAATTTAT 8889
 QY 181 AAATGAGCAAAATAT 194
 DB 8890 AAATGAGCAAAATAT 8903

RESULT 10

ID AAA50174 standard; DNA; 9721 BP.
 AC AAA50174;

DT 07-NOV-2000 (first entry)

DE Human interleukin-1 beta allele 1 (+6912).

XX Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;
 KW coronary artery disease; osteoporosis; nephropathy;
 KW alopecia areata; Graves disease; systemic lupus erythematosus;
 KW lichen sclerosus; ulcerative colitis; diabetic retinopathy;
 KW periodontal disease; juvenile chronic arthritis; psoriasis;
 KW insulin dependent diabetes; asthma; lung fibrosis;
 KW chronic inflammatory liver disease; rheumatoid arthritis;
 KW chronic inflammatory liver disease; antiinflammatory; osteopathic;
 KW dermatological; immunosuppressive; antidiabetic; antihypertensive;
 KW arthritic; antirheumatic; antiasthmatic; antipsoriatic;
 KW hepatotropic; antitumor; diagnosis; therapy; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH variation replace(8904,G)
 FT /*Tag= a
 FT /note= "IL-1B allele 1 (+6912)"

XX WO200047619-A1.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03443.

XX 10-FEB-1999; 99US-0247874.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Duff GW, Di Giovine FS;

XX WPI; 2000-558192/51.

XX Novel methods and nucleic acids for diagnosing and treating disorders
 PT associated with high levels of interleukin 1beta, especially
 PT inflammatory diseases -

XX Disclosure; Fig 1; 74pp; English.

XX The present sequence is that of human interleukin-1 beta (IL-1B)
 CC allele 1 (+6912), which is a form of the IL-1B gene that contains
 CC cytosine at position +6912; IL-1B allele 2 (+6912) has guanine at
 CC this position (see AAA50175). The invention is based on the
 CC identification of this novel allele at marker +6912 of the IL-1B
 CC gene. The C to G transition occurs within the 3' untranslated
 CC region of the IL-1B gene and results in an increased level of IL-1B
 CC protein. Individuals homozygous for the IL-1B allele 2 (+6912)
 CC accumulate approximately 4 times more immunoreactive IL-1B protein
 CC than homozygotes for IL-1B allele 1 (+6912). Methods and kits are
 CC provided for detecting IL-1B allele 2 (+6912), or an allele in
 CC linkage disequilibrium with an IL-1B allele 2 (+6912), and
 CC thereby determining a patient's susceptibility to developing
 CC inflammatory disorders, especially coronary artery disease,

CC osteoporosis, nephropathy in diabetes mellitus, alopecia areata,
 CC graves disease, systemic lupus erythematosus, lichen sclerosus,
 CC ulcerative colitis, diabetic retinopathy, periodontal disease,
 CC juvenile chronic arthritis, psoriasis, insulin dependent diabetes,
 CC asthma, chronic inflammatory liver disease, chronic inflammatory
 CC lung disease, lung fibrosis, and rheumatoid arthritis (claimed).
 CC Identification of the IL-1B allele 2 (+6912) and its involvement in
 CC IL-1B overproduction also enables screening assays for identifying
 CC IL-1B antagonists that can be used to treat conditions associated
 CC with IL-1B allele 2 (+6912). Transgenic animals are also claimed,
 CC and can be used to identify IL-1B agonists and antagonists, or
 CC to confirm the safety and efficacy of candidate therapeutics.

XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

QY Query Match 82.2%; Score 194; DB 21; Length 9721;
 DB Best Local Similarity 100.0%; Pred. NO. 1.3e-85;
 DB Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTGCTGCTTAATTTATTTCAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 60

DB 8710 TTTTGATTGCTGCTTAATTTATTTCAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 8769

QY 61 GCTAGTTTTTAATAGCTATGAATCAATTAATTGAGCTGGTGTCTCTTTAAATC 120

DB 8770 GCTAGTTTTTAATAGCTATGAATCAATTAATTGAGCTGGTGTCTCTTTAAATC 8829

QY 121 AAGTCCTTTAAATTAAGACTCAAAATATATAAGCTCAGATTATTAAATGGGAATTTAT 180

DB 8830 AAGTCCTTTAAATTAAGACTCAAAATATATAAGCTCAGATTATTAAATGGGAATTTAT 8889

QY 181 AAATGAGCAAAATAT 194

DB 8890 AAATGAGCAAAATAT 8903

RESULT 11

AAA34823
 ID AAA34823 standard; DNA; 9721 BP.

XX AAA34823;

XX 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:2512.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,

XX 24-MAY-2000; 2000WO-US14299.
XX
XX
PR 24-MAY-1999; 99US-0317674.
PR 01-NOV-1999; 99US-0431352.
XX
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
XX
PI Kornman KS, Duff GW, Crossman DC, Francis SE, Stephenson K;
XX
XX WPI; 2001-025173/03.
DR
XX
XX
PT Diagnosing or determining susceptibility to developing restenosis
PT involves detecting restenosis associated allele in a nucleic acid
PT sample -
XX
XX Disclosure; Fig 2; 129pp; English.
XX
XX The present sequence is given in a specification relating to a method for
XX determining whether a subject has or is predisposed to developing an
XX arterial restenosis. The method comprises detecting a restenosis
XX associated allele (RAA) in a nucleic acid sample from the subject, where
XX detection of the RAA indicates that the subject has or is predisposed to
XX the development of a restenosis. The restenosis associated allele
XX pattern permits the diagnosis of occlusive cardiovascular disorder. The
XX diagnosis allows the most suitable treatment methods for restenosis to be
XX used e.g. selecting therapies for initial vascular stenosis most likely
XX to avoid subsequent stenoses. The detection methods identify restenosis
XX therapeutics, agonists and antagonists (proteins, peptides,
XX peptidomimetics, small molecules or nucleic acids, e.g. anti-sense,
XX ribozyme and triplex nucleic acids) which are used to treat restenosis.
XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
Query Match 82.2%; Score 194; DB 22; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATGGTCTAATTATTCAAAAGGGGCAAGAGTAGCAGTCTGTAAAAGA 60
DB 8710 TTTTGATTCAATGGTCTAATTATTCAAAAGGGGCAAGAGTAGCAGTCTGTAAAAGA 8769
QY 61 GCCTAGTTTTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 120
DB 8770 GCCTAGTTTTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 8829
QY 121 AAGTCCITTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 180
DB 8830 AAGTCCITTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 8889
QY 181 AAATGAGCAAAATAT 194
DB 8890 AAATGAGCAAAATAT 8903
RESULT 14
AAD35192
ID AAD35192 standard; DNA; 9721 BP.
XX
XX AAD35192;
XX
XX
DT 25-JUL-2002 (first entry)
XX
XX Human prointerleukin-1 beta (IL-1 beta) gene.
XX
XX Unexplained recurrent pregnancy loss; immunologic reproductive failure;
XX URPL; prointerleukin-1beta; IL-1beta; human; ds.
XX
XX Homo sapiens.
XX
XX WO20022877-A2.
XX
XX 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US28465.
XX
XX
PR 12-SEP-2000; 2000US-231785P.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX (DAND) DANA FARBER CANCER INST INC.
XX
XX Hill JA, Wang ZC, Anderson DJ, Yunis EJ;
XX
XX WPI; 2002-362362/39.
DR
XX
XX Evaluating risk of unexplained recurrent pregnancy loss in a subject,
PT by testing presence of a variant in interleukin-1 beta promoter region
PT and/or in CD46 gene intron 1 region in a sample obtained from the
PT subject -
XX
XX Example 2 and 3; Page 51-54; 57pp; English.
XX
XX The invention relates to a method for evaluating and treating risk of
XX unexplained recurrent pregnancy loss (URPL) in a subject suspected of
XX having immunologic reproductive failure. The method involves testing a
XX sample obtained from the subject for the presence of a variant in the
XX human interleukin-1beta (IL-1beta) promoter region, and/or a variant
XX in the CD46 gene intron 1 region, where the presence of the variant,
XX indicates an elevated risk of developing recurrent pregnancy loss.
XX The present sequence is human prointerleukin-1 beta (IL-1 beta) gene.
XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
Query Match 82.2%; Score 194; DB 24; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATGGTCTAATTATTCAAAAGGGGCAAGAGTAGCAGTCTGTAAAAGA 60
DB 8710 TTTTGATTCAATGGTCTAATTATTCAAAAGGGGCAAGAGTAGCAGTCTGTAAAAGA 8769
QY 61 GCCTAGTTTTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 120
DB 8770 GCCTAGTTTTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 8829
QY 121 AAGTCCITTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 180
DB 8830 AAGTCCITTTAATGACTATGGAATCAATTCAAATTGGACTGGTGTCTCTTTAAATC 8889
QY 181 AAATGAGCAAAATAT 194
DB 8890 AAATGAGCAAAATAT 8903
RESULT 15
AAF20950
ID AAF20950 standard; DNA; 29433 BP.
XX
XX AAF20950;
XX
XX
DT 14-MAR-2001 (first entry)
XX
XX Human interleukin-1 polynucleotide fragment #2517.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antialsthmatic; analgesic; hypotensive; cycostatic;
KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
KW surfactant hypoproduction; pulmonary fibrosis; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
XX
XX OS

Search completed: March 17, 2003, 20:46:15
Job time : 257 secs

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XX WO200062736-A2.
XX
XX PD 26-OCT-2000.
XX
XX PF 24-MAR-2000; 2000WO-US08020.
XX
XX PR 06-APR-1999; 99US-0127958.
XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX
XX PI Nyce JW;
XX
XX DR WPI; 2000-679539/66.
XX
XX PT Low adenosine (A) content antisense oligonucleotides which do not
XX PT trigger adenosine receptors during metabolism, useful e.g. for treating
XX PT cancers and respiratory obstructions -
XX
XX PS Disclosure; Page 221-227; 1592pp; English.
XX
XX CC The present invention describes low adenosine (A) content antisense
XX CC oligonucleotides and compositions (I) comprising them. In the antisense
XX CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX CC The antisense oligonucleotides and (I) can be used to down-regulate the
XX CC expression and or activity of target polypeptides associated with
XX CC lung/respiratory disorders and malignancies, such as stimulating and
XX CC activating peptide factors and transmitters, transcription factors,
XX CC immunoglobulins and antibodies, antibody receptors, cytokines and
XX CC chemokines, endogenously produced specific and non-specific enzymes,
XX CC binding proteins, adhesion molecules and their receptors, cytokine and
XX CC chemokine receptors, adenosine receptors, bradykinin receptors, central
XX CC nervous system (CNS) and peripheral nervous and non-nervous system
XX CC receptors, CNS and peripheral nervous and non-nervous system peptide
XX CC transmitters, defensins, growth factors, vasoactive peptides and
XX CC receptors, binding proteins and malignancy associated proteins. The
XX CC antisense oligonucleotides may be used in this way to treat disorders
XX CC including respiratory obstruction (especially pulmonary obstruction
XX CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
XX CC and/or surfactant hypoproduction which are associated with a disease or
XX CC condition selected from pulmonary vasoconstriction, inflammation
XX CC allergies, asthma, impeded respiration, respiratory distress syndrome
XX CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX CC fragments and antisense oligonucleotides used in the exemplification of
XX CC the present invention.
XX
XX SQ Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 2 other;
Query Match 82.2%; Score 194; DB 21; Length 29433;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTGCTGGTCTTAATTATTCAAAGGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60
DB 22177 TTTTGATTGCTGGTCTTAATTATTCAAAGGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 22236
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTCTTTAAATC 120
DB 22237 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTCTTTAAATC 22296
QY 121 AAGTCCTTTAATAAGACTGAAATATATATAGCTCAGATTATTTAAATGGGAATATTAT 180
DB 22297 AAGTCCTTTAATAAGACTGAAATATATATAGCTCAGATTATTTAAATGGGAATATTAT 22356
QY 181 AAATGAGCAATAT 194
DB 22357 AAATGAGCAATAT 22370
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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 20:34:55 ; Search time 1462 Seconds
(without alignments)
2614.319 Million cell updates/sec

Title: US-09-247-874c-2_COPY_8710_8945
Perfect score: 236
Sequence: 1 ttttgattcattggtctaat.....ataaacttcactgaagaaaa 236

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estnu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_htc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: gb_gss.*
- 18: em_gss_hum.*
- 19: em_gss_inv.*
- 20: em_gss_pln.*
- 21: em_gss_vrt.*
- 22: em_gss_fun.*
- 23: em_gss_mam.*
- 24: em_gss_mus.*
- 25: em_gss_other.*
- 26: em_gss_pro.*
- 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	189	80.1	324	9	AA923615
C 2	189	80.1	413	14	W36319
C 3	189	80.1	514	9	AA131744
C 4	189	80.1	521	9	AI022364
C 5	189	80.1	528	9	AI678441
C 6	189	80.1	548	14	BM997237

C 7	189	80.1	554	9	AA577318
C 8	189	80.1	618	10	AA273081
C 9	189	80.1	703	14	BQ001221
C 10	189	80.1	770	14	BQ000281
C 11	189	80.1	817	9	AI609005
C 12	189	80.1	911	12	BG194765
C 13	147	62.3	549	9	AI566931
C 14	147	62.3	746	13	BI519707
C 15	143	60.6	793	14	BM999417
C 16	138	58.5	314	9	AA382165
C 17	138	58.5	375	12	BG119263
C 18	138	58.5	698	9	AI471571
C 19	136	57.6	429	14	T29172
C 20	130	55.1	415	9	AA362146
C 21	130	55.1	749	12	BG117168
C 22	125	53.0	454	14	D20737
C 23	124	52.5	223	9	AA362379
C 24	113	47.9	619	10	AW953756
C 25	108	45.8	430	14	W47101
C 26	107	45.3	196	9	AA362067
C 27	97	41.1	241	14	C06317
C 28	93	39.4	286	10	BE183186
C 29	61	25.8	925	10	BE619601
C 30	51	21.6	252	10	AW779422
C 31	31	13.1	259	12	EG058513
C 32	28	11.9	265	10	BE183137
C 33	24	10.2	703	10	AV715551
C 34	23	9.7	360	9	AA916006
C 35	22	9.3	559	17	BH598295
C 36	20	8.5	685	17	AG163910
C 37	20	8.5	993	17	CNS060CR
C 38	19	8.1	300	14	C53301
C 39	19	8.1	381	17	A2236878
C 40	19	8.1	463	13	BJ148984
C 41	19	8.1	476	14	BM664065
C 42	19	8.1	583	17	BH674814
C 43	19	8.1	616	17	AQ436473
C 44	19	8.1	646	12	BG09864
C 45	19	8.1	661	10	AV702246

ALIGNMENTS

RESULT 1
AA923615/c 324 bp mRNA linear EST 29-APR-1998
LOCUS nc98b03.s1 NCI CGAP Col0 Homo sapiens cDNA clone IMAGE:1160333 3,
DEFINITION similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AA923615
VERSION AA923615.1 GI:3070924
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1123 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 214.

FEATURES

Location/Qualifiers
1..324
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1160333"
/clone.lib="NCI CGAP Col0"
/tissue_type="Colon Tumor RER-4"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - Rligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."

BASE COUNT

117 a 55 c 57 g 95 t

ORIGIN

Query Match 80.1%; Score 189; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 7e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCAATGGTCTAATTTATTCACAGGGGCGAAGTAGCAGTGTCTGTAAGAGGCTTA 65
Db 227 ATTCATTTGGTCTAATTTATTCACAGGGGCGAAGTAGCAGTGTCTGTAAGAGGCTTA 168
QY 66 GTTTTAAATAGCTAGGATCAATTCATTTGGACTGTGTCTCTTTAAATCAAGTC 125
Db 167 GTTTTAAATAGCTAGGATCAATTCATTTGGACTGTGTCTCTTTAAATCAAGTC 108
QY 126 CTTTAAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGGAATATTTATAATG 185
Db 107 CTTTAAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGGAATATTTATAATG 48
QY 186 AGCAAAATAT 194
Db 47 AGCAAAATAT 39

RESULT 2

W38319/c 413 bp mRNA linear EST 15-MAY-1996
LOCUS zc77b02.sl Pancreatic Islet Homo sapiens cDNA clone IMAGE:328299 3'
DEFINITION similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA
sequence.
ACCESSION W38319
VERSION W38319.1 GI:1319934
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

TITLE Washington University School of Medicine
JOURNAL 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
MEDLINE Tel: 314 286 1800
Contact: Wilson RK Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET
High quality sequence stop: 368.

FEATURES

Location/Qualifiers
1..413
/organism="Homo sapiens"
/db_xref="GDB:1262503"
/db_xref="taxon:9606"
/clone="IMAGE:328299"
/clone.lib="Pancreatic Islet"
/tissue_type="pancreatic islet"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1. SCORI; Site 2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993) Takeda et al. Cloned unidirectionally. Primer: Oligo dt. -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'

BASE COUNT 135 a 65 c 86 g 127 t

ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 413;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTTGGTCTAATTTATTCACAGGGGCGAAGTAGCAGTGTCTGTAAGAGGCTTA 65
Db 239 ATTCATTTGGTCTAATTTATTCACAGGGGCGAAGTAGCAGTGTCTGTAAGAGGCTTA 180
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGTGTCTCTTTAAATCAAGTC 125
Db 179 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGTGTCTCTTTAAATCAAGTC 120
QY 126 CTTTAAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGGAATATTTATAATG 185
Db 119 CTTTAAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGGAATATTTATAATG 60
QY 186 AGCAAAATAT 194
Db 59 AGCAAAATAT 51

RESULT 3

AA131744/c 514 bp mRNA linear EST 27-NOV-1996
LOCUS z135f02.sl Soares pregnant uterus NCHPU Homo sapiens cDNA clone
DEFINITION IMAGE:503931 3' similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA sequence.
ACCESSION AA131744
VERSION AA131744.1 GI:1693270
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 514)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisan,E., Waterston,R., Wohlmann,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK

TITLE Washington University School of Medicine
JOURNAL 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
MEDLINE Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 277.

FEATURES

Location/Qualifiers
1..514
/organism="Homo sapiens"


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/db_xref="GB9:3808919"
/db_xref="taxon:9606"
/clone="IMAGE:503931"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: pT73-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5, AACTGGAAGATTGGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
BASE COUNT 156 a 85 c 114 g 149 t 10 others
ORIGIN
Query Match 80.1%; Score 189; DB 9; Length 514;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 244 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 185
|||||
QY 66 GTTTTAAATAGCTATGGAATCAATTTCGACTGGTGCTCTCTTTAAATCAAGTC 125
|||||
Db 184 GTTTTAAATAGCTATGGAATCAATTTCGACTGGTGCTCTCTTTAAATCAAGTC 125
|||||
QY 126 CTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
|||||
Db 124 CTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 65
|||||
QY 186 AGCAAAATAT 194
|||||
Db 64 AGCAAAATAT 56

RESULT 4
AI022364/c
LOCUS
DEFINITION ow64g05.x1 Soares senescent fibroblasts NDHSF Homo sapiens cDNA clone IMAGE:1651640 3', similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI022364
VERSION AI022364.1 GI:3237605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 521)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1077 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 403.
Location/Qualifiers
1..521
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1651640"
/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"

/note="Vector: pT73D (Pharmacia) with a modified polylinker V-TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5, TGTACCAATCTGAAGTGGGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 165 a 92 c 123 g 141 t
ORIGIN
Query Match 80.1%; Score 189; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 232 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 173
|||||
QY 66 GTTTTAAATAGCTATGGAATCAATTTCGACTGGTGCTCTCTTTAAATCAAGTC 125
|||||
Db 172 GTTTTAAATAGCTATGGAATCAATTTCGACTGGTGCTCTCTTTAAATCAAGTC 113
|||||
QY 126 CTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
|||||
Db 112 CTTTAAATTAAGCTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 53
|||||
QY 186 AGCAAAATAT 194
|||||
Db 52 AGCAAAATAT 44

RESULT 5
AI078441/c
LOCUS
DEFINITION tu82d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2257537 3', similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI078441
VERSION AI078441.1 GI:4888623
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1763 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 404.
Location/Qualifiers
1..528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2257537"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with source

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signet ring cell features"

/lab host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

BASE COUNT 172 a 98 c 117 g 140 t 1 others
ORIGIN
Query Match 80.1%; Score 189; DB 9; Length 528;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
Db 227 ATTCATTGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 168
QY 66 GTTTTAAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
Db 167 GTTTTAAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 108
QY 126 CTTTAAATTAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 185
Db 107 CTTTAAATTAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 48
QY 186 AGCAATAT 194
Db 47 AGCAATAT 39

RESULT 6

BM997237/5
LOCUS BM997237 548 bp mRNA linear EST 17-JUN-2002
DEFINITION UI-H-DHO-auc-f-03-0-UI.s1 NCI_CGAP_DHO Homo sapiens cDNA clone
IMAGE:5872130 3', mRNA sequence.

ACCESSION BM997237
VERSION BM997237.1 GI:19722138

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 548)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

UNPUBLISHED (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA

sequence: 221-272, >(TAAA)n#simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..548

/organism="Homo sapiens"

/db xref="taxon:9606"

/clones="IMAGE:5872130"

/clone_lib="NCI CGAP DHO"

/tissue_type="Metastatic Chondrosarcoma"

/dev_stage="Adult"

/lab_hosts="DH10B (Life Technologies)"

/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP DHO is a cDNA library containing the following

tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma

in Lung. The library was constructed according to Bonaldo,

Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor digested with Not I, and cloned
directionally into p773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGATCATTCG.

TAG LIB=UI-H-DHO

TAG_TISSUE=Lung

TAG_SEQ=AGATCATTCG

BASE COUNT 172 a 95 c 123 g 158 t

ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 548;
Best Local Similarity 100.0%; Pred. No. 7.5e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
Db 242 ATTCATTGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 183
QY 66 GTTTTAAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
Db 182 GTTTTAAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 123
QY 126 CTTTAAATTAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 185
Db 122 CTTTAAATTAAGCTAGTGGATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 63
QY 186 AGCAATAT 194
Db 62 AGCAATAT 54

RESULT 7

AA577318/c

LOCUS AA577318

DEFINITION nm89a08.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1075382 3'

similar to gb:IM15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA

sequence.

ACCESSION AA577318

VERSION AA577318.1 GI:2354792

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 554)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

UNPUBLISHED (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,

Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1351 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 414.

Location/Qualifiers

1..554

/organism="Homo sapiens"

/db xref="taxon:9606"

/clones="IMAGE:1075382"

/clone_lib="NCI_CGAP_C09"

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/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo (Soares4
)."
BASE COUNT 176 a 97 c 126 g 154 t 1 others
ORIGIN

Query Match 80.1%; Score 189; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 7.5e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTCAAGGGGGCAAGAGTAGCAGTCTGTAAAGAGCCTA 65
Dd 231 ATTCATTGGTCTAATTATTCAAGGGGGCAAGAGTAGCAGTCTGTAAAGAGCCTA 172
QY 66 GTTTTAAATAGCTATGGAATCAATTGGAATTTGGAATGTTGCTCTCTTTAAATCAAGTC 125
Dd 171 GTTTTAAATAGCTATGGAATCAATTGGAATTTGGAATGTTGCTCTCTTTAAATCAAGTC 112
QY 126 CTTTAAATAGCTATGGAATCAATTGGAATTTGGAATTTTAAATGGAATATTTTAAATG 185
Dd 111 CTTTAAATAGCTATGGAATCAATTGGAATTTGGAATTTTAAATGGAATATTTTAAATG 52
QY 186 AGCAAAATAT 194
Dd 51 AGCAAAATAT 43

RESULT 8
AW273081/c
LOCUS
DEFINITION xu27h01.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2801425 3', mRNA
similar to gb:M5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AW273081
VERSION AW273081.1 GI:6660111
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 618)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 399.
Location/Qualifiers
1..618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2801425"
/clone_lib="NCI_CGAP_Col4"

FEATURES
source
```

```
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
BASE COUNT 193 a 121 c 137 g 167 t
ORIGIN

Query Match 80.1%; Score 189; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 7.6e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTCAAGGGGGCAAGAGTAGCAGTCTGTAAAGAGCCTA 65
Dd 227 ATTCATTGGTCTAATTATTCAAGGGGGCAAGAGTAGCAGTCTGTAAAGAGCCTA 168
QY 66 GTTTTAAATAGCTATGGAATCAATTGGAATTTGGAATGTTGCTCTCTTTAAATCAAGTC 125
Dd 167 GTTTTAAATAGCTATGGAATCAATTGGAATTTGGAATGTTGCTCTCTTTAAATCAAGTC 108
QY 126 CTTTAAATAGCTATGGAATCAATTGGAATTTTAAATGGAATATTTTAAATG 185
Dd 107 CTTTAAATAGCTATGGAATCAATTGGAATTTTAAATGGAATATTTTAAATG 48
QY 186 AGCAAAATAT 194
Dd 47 AGCAAAATAT 39

RESULT 9
BQ001221/c
LOCUS
DEFINITION UI-H-DH1-awp-g-21-0-UI-s1 NCI CGAP DH1 Homo sapiens cDNA clone
IMAGE:5892524 3', mRNA sequence.
ACCESSION BQ001221
VERSION BQ001221.1 GI:19726121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 703)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n$Simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers
1..703
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5892524"
/clone_lib="NCI_CGAP_DH1"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI-CGAP DH1 is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in lung. The library was constructed
```

according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p77T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTCG.

TAG LIB=UI-H-DH1

TAG_TISSUE=lung

TAG_SEQ=AGATCATTCG

BASE COUNT 203 a 139 c 158 g 202 t 1 others

ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 703;

Best Local Similarity 100.0%; Pred. No. 7.7e-93;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCAATGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65

Db 242 ATTCAATGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 183

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 10

BQ000281/c

LOCUS

DEFINITION

UI-H-DP0-avt-c-13-0-UI.sl NCI_CGAP_Fs1 Homo sapiens cDNA clone

IMAGE:5883972 3', mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 10

BQ000281/c

LOCUS

DEFINITION

UI-H-DP0-avt-c-13-0-UI.sl NCI_CGAP_Fs1 Homo sapiens cDNA clone

IMAGE:5883972 3', mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 10

BQ000281/c

LOCUS

DEFINITION

UI-H-DP0-avt-c-13-0-UI.sl NCI_CGAP_Fs1 Homo sapiens cDNA clone

IMAGE:5883972 3', mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 10

BQ000281/c

LOCUS

DEFINITION

UI-H-DP0-avt-c-13-0-UI.sl NCI_CGAP_Fs1 Homo sapiens cDNA clone

IMAGE:5883972 3', mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

/note="Vector: p77T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_Fs1 is a cDNA library containing the following tissue(s): Fibrosarcoma Cell line HT-1080 (ATCC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p77T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTCTACGAG.

TAG LIB=UI-H-DP0

TAG_TISSUE=fibrosarcoma

TAG_SEQ=GTTCTACGAG

BASE COUNT 218 a 148 c 177 g 224 t 3 others

ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 770;

Best Local Similarity 100.0%; Pred. No. 7.8e-93;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCAATGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65

Db 242 ATTCAATGCTCTTAATTTATTCAGAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 183

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

AI609005 817 bp mRNA linear EST 15-DEC-1999
tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

AI609005 GI:4618172

AI609005

EST

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 817)

NCI/NIH-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute / National Institute of Dental Research,

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Chong Heon Lee, D.D.S., Mary May, J. Silvio

Guckind, Ph.D., Myung Hee Park, Ph.D.

cDNA Library Preparation: Stratagene, Inc.

cDNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 1651 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 441

POLYA=No.

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

Db 122 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 63

QY 186 AGCAATAT 194

Db 62 AGCAATAT 54

RESULT 11

AI609005/c

LOCUS

DEFINITION

tw85907.x1 NCI CGAP HNS Homo sapiens cDNA clone IMAGE:2266524 3', similar to GB:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

QY 66 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 125

Db 182 GTTTTAAATAGCTATGGATCAATTCATTTGGAGCTGTCTCTCTTTAAATCAAGTC 123

QY 126 CTTTAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGATATTTTATAATG 185

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FEATURES
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        /clone_xref="IMAGE:2266524"
        /clone_lib="NCI_CGAP_HN5"
        /tissue_type="normal gingiva (cell line from primary
        keratinocytes)"
        /lab_host="SOLR (kanamycin resistant)"
        /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI
        ; Cloned unidirectionally. Primer: Oligo dt. Average
        insert size 1.3 kb. 5' adaptor sequence: 5' AATTCGGACGAG
        3' GCCGTGCTC 5' 3' adaptor sequence: 5' AATTCGGACGAG
        3' (GA)10ACTAGCTCGAGTTTTTTTTTTTTTTT 3' EcoRI
        site appears to have been lost in a fraction of the
        clones. Library constructed by Stratagene; available
        through Mary May, PhD (Oral and Pharyngeal Cancer Branch,
        National Institute of Dental and Craniofacial Research,
        NIH; mmay@yoda.nidrr.nih.gov)."
      BASE COUNT 230 a 163 c 187 g 231 t 6 others
      ORIGIN
        Query Match 80.1%; Score 189; DB 9; Length 817;
        Best Local Similarity 100.0%; Pred. No. 7.9e-93;
        Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        QY 6 ATTCATTGGTCTTAATTTATTCACAGGGGGCAAGTAGCAGTGTCTGTTAAAGAGCCTA 65
        Db 229 ATTCATTGGTCTTAATTTATTCACAGGGGGCAAGTAGCAGTGTCTGTTAAAGAGCCTA 170
        QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
        Db 169 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 110
        QY 126 CTTTAAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
        Db 109 CTTTAAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 50
        QY 186 AGCAAAATAT 194
        Db 49 AGCAAAATAT 41
      RESULT 12
      BG194765/c
      LOCUS BG194765 911 bp mRNA linear EST 21-APR-2001
      DEFINITION BG194765 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
      ACCESSION BG194765.1 GI:13716580
      VERSION BG194765.1
      KEYWORDS EST.
      SOURCE human.
      ORGANISM Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 911)
      HARRINGTON,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
      CAIN,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
      Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
      ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
      ,J., Danzig,J. and Ducar,M.
      Creation of genome-wide protein expression libraries using random
      activation of gene expression
      Nat. Biotechnol. 19 (5), 440-445 (2001)
      21227151
      CONTACT: Scott J. Cain
      Athersys, Inc.
      3201 Carnegie Ave, Cleveland, OH 44115, USA
      Tel: 216 431 9900
      Fax: 216 361 9596
      Email: scain@atersys.com
      High quality sequence stop: 434.
      Location/Qualifiers
        1..911
      FEATURES
        source
          Location/Qualifiers
            1..549
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_xref="IMAGE:2213907"
              /clone_lib="NCI_CGAP_Lu19"
              /tissue_type="squamous cell carcinoma, poorly

```

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 254 a 184 c 219 g 254 t
ORIGIN
  Query Match 80.1%; Score 189; DB 12; Length 911;
  Best Local Similarity 100.0%; Pred. No. 8e-93;
  Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 6 ATTCATTGGTCTTAATTTATTCACAGGGGGCAAGTAGCAGTGTCTGTTAAAGAGCCTA 65
  Db 229 ATTCATTGGTCTTAATTTATTCACAGGGGGCAAGTAGCAGTGTCTGTTAAAGAGCCTA 170
  QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
  Db 169 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 110
  QY 126 CTTTAAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
  Db 109 CTTTAAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 50
  QY 186 AGCAAAATAT 194
  Db 49 AGCAAAATAT 41

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RESULT 13
AI566931/c
LOCUS AI566931 549 bp mRNA linear EST 13-MAY-1999
DEFINITION tq67h02.x1 NCI_CGAP Lu19 Homo sapiens cDNA clone IMAGE:2213907 3'
similar to gb:IM15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AI566931
VERSION AI566931.1 GI:4525383
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 549)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1104 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 409
POLYA=No.
FEATURES
  source
    Location/Qualifiers
      1..549
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_xref="IMAGE:2213907"
        /clone_lib="NCI_CGAP_Lu19"
        /tissue_type="squamous cell carcinoma, poorly

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differentiated (4 pooled tumors, including primary and metastatic)"
 /dev stages="adult"
 /lab host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dN) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 173 a 107 c 119 g 149 t 1 others
 ORIGIN
 Query Match 62.3%; Score 147; DB 9; Length 549;
 Best Local Similarity 100.0%; Pred. No. 9.1e-70;
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 48 TGTCTGTAAGAGCCTAGTCTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTG 107
 DB 186 TGTCTGTAAGAGCCTAGTCTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTG 127
 QY 108 CTCTCTTTAAATCAAGTCTTTTAAATAGACTGAAATATATAGCTCAGATTATTTAAA 167
 DB 126 CTCTCTTTAAATCAAGTCTTTTAAATAGACTGAAATATATAGCTCAGATTATTTAAA 67
 QY 168 TGGGAATTTATTAATGAGCAATAT 194
 DB 66 TGGGAATTTATTAATGAGCAATAT 40

RESULT 14
 B1519707/c
 LOCUS B1519707 746 bp mRNA linear EST 29-AUG-2001
 DEFINITION 603061928T1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211294 3', mRNA sequence.
 ACCESSION B1519707
 VERSION B1519707.1 GI:15344499
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 746)
 NTH-MGC http://mgc.ncbi.nlm.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: L1AM11530 row: g column: 07
 High quality sequence start: 3
 High quality sequence stop: 740.

FEATURES
 source
 1. 746
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="IMAGE:5211294"
 /clone_lib="NIH_MGC_118"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
 BASE COUNT 206 a 158 c 177 g 205 t
 ORIGIN

Query Match 62.3%; Score 147; DB 13; Length 746;
 Best Local Similarity 100.0%; Pred. No. 9.5e-70;
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ATTCAATGCTCTAATTTATTCAAAGGGGCAAGACAGTAGCTGTGTAAGAAGCCTTA 65
 DB 148 ATTCAATGCTCTAATTTATTCAAAGGGGCAAGACAGTAGCTGTGTAAGAAGCCTTA 89
 QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
 DB 88 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 29
 QY 126 CTTTAATTAAGACTGAAATATATATAAG 152
 DB 28 CTTTAATTAAGACTGAAATATATAAG 2

RESULT 15
 BM999417/c
 LOCUS BM999417 793 bp mRNA linear EST 17-JUN-2002
 DEFINITION UI-H-DFO-avf-1-11-0-UI-s1 NCI_CGAP_Fs1 Homo sapiens cDNA clone IMAGE:5878810 3', mRNA sequence.
 ACCESSION BM999417
 VERSION BM999417.1 GI:19724318
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 793)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Mary Hendrix
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA sequence: 219-270, >(TAAA)n#simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 Location/Qualifiers
 1. 793
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="IMAGE:5878810"
 /clone_lib="NCI_CGAP_Fs1"
 /tissue_type="Fibrosarcoma"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_Fs1 is a cDNA library containing the following tissue(s): Fibrosarcoma Cell line HT-1080 (ATCC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains

a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTCTACGAG.

TAG LIB=UI-H-DPO
TAG TISSUE=fibrosarcoma
TAG SEQ=GTTCTACGAG"

BASE COUNT 224 a 154 c 181 g 231 t 3 others
ORIGIN

Query Match 60.8%; Score 143; DB 14; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.5e-67;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ATTCATTGGTCTAATTATTCAAGGGGGCAAGTAGCAGTGTCTGTAAGAGCCCTA 65

Db 240 ATTCATTGGTCTAATTATTCAAGGGGGCAAGTAGCAGTGTCTGTAAGAGCCCTA 181

Qy 66 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTGCTCTCTTTAAATCAAGTC 125

Db 180 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTGCTCTCTTTAAATCAAGTC 121

Qy 126 CTTTAATTAGACTGAAATATA 148

Db 120 CTTTAATTAGACTGAAATATA 98

Search completed: March 17, 2003, 21:29:38
Job time : 1464 secs

